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## Shears, Beverly

---

**From:** Hamud, Fozia  
**Sent:** Monday, August 18, 2003 12:36 PM  
**To:** Shears, Beverly  
**Subject:** RE: Seq. Search Request

Sorry about that. It is SEQ ID NO:2. Thanks.

-----Original Message-----

**From:** Shears, Beverly  
**Sent:** Monday, August 18, 2003 12:34 PM  
**To:** Hamud, Fozia  
**Subject:** Seq. Search Request

Fozia,

You recently submitted a seq. search request for SN 09/892949; however, you omitted the Seq. ID to be searched. Your request reads:

*Pls. search SEQ ID NO:from amino acid residue 20-227; 544-732; 520-543 against commercial data bases. thanks.*

Which Seq. ID do you wish to search?

BEVERLY SHEARS  
USPTO  
BIOTECH/CHEM LIBRARY  
CM-1, RM 1E05  
703-308-4994  
BEVERLY.SHEARS@USPTO.GOV

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Hamud F.  
09/892449 Page 1  
Seq. ID 2GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:12:37 ; Search time 79.0499 Seconds  
(without alignments)  
417.649 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_20\_227

Perfect score: 1121  
Sequence: 1 ALPAKRENTSCVYYRKRLT.....SKFWSDSQEKMGTEEEAP 208Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1984.DAT:*
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7: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1987.DAT:*
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11: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1991.DAT:*
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18: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 1121  | 100.0       | 324    | ABB05732 | Zcytor17 soluble f |
| 2          | 1121  | 100.0       | 548    | ABP54369 | Human NR10.8 splic |
| 3          | 1121  | 100.0       | 549    | ABP54368 | Human NR10.7 splic |
| 4          | 1121  | 100.0       | 581    | ABP54367 | Human NR10.6 splic |
| 5          | 1121  | 100.0       | 582    | ABP54368 | Human angiotensin  |
| 6          | 1121  | 100.0       | 582    | ABP54368 | Human PRO21384 pro |
| 7          | 1121  | 100.0       | 582    | AAU83637 | Human PRO protein, |
| 8          | 1121  | 100.0       | 627    | ABP54366 | Human NR10.5 splic |
| 9          | 1121  | 100.0       | 649    | ABB05738 | Human zcytor17 pro |

|    |       |       |     |    |          |                    |
|----|-------|-------|-----|----|----------|--------------------|
| 10 | 1121  | 100.0 | 652 | 22 | AAE24022 | Human haemopoietin |
| 11 | 1121  | 100.0 | 652 | 23 | AAE24028 | Human HPR1 variant |
| 12 | 1121  | 100.0 | 662 | 22 | AAE24024 | Human haemopoietin |
| 13 | 1121  | 100.0 | 662 | 23 | AAE24029 | Human HPR1 variant |
| 14 | 1121  | 100.0 | 662 | 23 | ABP54369 | Human zcytor17 pro |
| 15 | 1121  | 100.0 | 681 | 24 | ABP54363 | Human NR10.3 splic |
| 16 | 1121  | 100.0 | 732 | 23 | ABP54363 | Human zcytor17 pro |
| 17 | 1121  | 100.0 | 745 | 23 | AAE24024 | Human haemopoietin |
| 18 | 1121  | 100.0 | 764 | 23 | ABP54363 | Human haemopoietin |
| 19 | 1121  | 100.0 | 764 | 24 | ABP54364 | Human NR10.4 splic |
| 20 | 1121  | 100.0 | 764 | 24 | ABP54365 | Human NR10.4 splic |
| 21 | 1110  | 99.0  | 239 | 23 | ABP54363 | Human zcytor17 pro |
| 22 | 1110  | 99.0  | 252 | 22 | ABP54363 | Human haemopoietin |
| 23 | 1110  | 99.0  | 252 | 23 | AAE24027 | Human HPR1 variant |
| 24 | 502.5 | 44.8  | 547 | 23 | ABP54363 | Mouse zcytor17 pro |
| 25 | 502.5 | 44.8  | 662 | 23 | ABP54363 | Mouse zcytor17 pro |
| 26 | 502.5 | 44.8  | 716 | 24 | ABP54371 | Mouse NR10B1b-C    |
| 27 | 502.5 | 44.8  | 716 | 24 | ABP54371 | Mouse NR10B1b-C    |
| 28 | 502.5 | 44.8  | 726 | 23 | AAE24037 | Mouse haemopoietin |
| 29 | 295   | 26.3  | 77  | 23 | AAE24022 | Human HPR1 protein |
| 30 | 271.5 | 24.2  | 917 | 13 | AAE24022 | Mouse gp130        |
| 31 | 271.5 | 24.2  | 917 | 13 | AAE24022 | Mouse gp130        |
| 32 | 268.5 | 24.0  | 332 | 20 | AAE24022 | Human gp130-delta  |
| 33 | 268.5 | 24.0  | 332 | 21 | AAE24022 | Human gp130-delta  |
| 34 | 268.5 | 24.0  | 332 | 21 | AAE24022 | Human gp130-delta  |
| 35 | 268.5 | 24.0  | 488 | 23 | AAE24022 | Human gp130-delta  |
| 36 | 268.5 | 24.0  | 658 | 17 | AAE24022 | Human gp130-delta  |
| 37 | 268.5 | 24.0  | 708 | 17 | AAE24022 | Human gp130-delta  |
| 38 | 268.5 | 24.0  | 727 | 21 | AAE24022 | Human gp130-delta  |
| 39 | 268.5 | 24.0  | 738 | 21 | AAE24022 | Human gp130-delta  |
| 40 | 268.5 | 24.0  | 809 | 23 | AAE24022 | Human gp130-delta  |
| 41 | 268.5 | 24.0  | 859 | 20 | AAE24022 | Human gp130-delta  |
| 42 | 268.5 | 24.0  | 859 | 21 | AAE24022 | Human gp130-delta  |
| 43 | 268.5 | 24.0  | 918 | 12 | AAE24022 | Human gp130-delta  |
| 44 | 268.5 | 24.0  | 918 | 15 | AAE24022 | Human gp130-delta  |
| 45 | 268.5 | 24.0  | 918 | 17 | AAE24022 | Human gp130-delta  |

## ALIGNMENTS

RESULT 1  
ABB05732  
ID ABB05732 standard; Protein, 324 AA.  
XX ABB05732;  
AC ABB05732;  
XX 01-MAY-2002 (first entry)  
XX DE  
XX Zcytor17 soluble form truncated in the fibronectin domain SEQ ID NO:18.  
XX DE  
XX Zcytor17, chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
XX anti-inflammation; antiviral; antileukemic; cytotoxic; bone;  
XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
XX infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
XX inflammatory disease; pancreatitis; inflammatory bowel disease.  
XX OS Homo sapiens.  
XX PN WO20020721-A2.  
XX PD 03-JAN-2002.  
XX PF 26-JUN-2001; 2001WO-US20484.  
XX PR 26-JUN-2000; 2000US-214282P.  
XX PR 29-JUN-2000; 2000US-214955P.  
XX PR 08-FEB-2001; 2001US-267963P.  
XX (ZIMO) ZYMOGENETICS INC.  
XX Sprecher CA, Presnell SR, Gao Z, Whitmore TB, Kujiiper JL,  
PI

PI Maurer MF;  
 XX WPI; 2002-090519/12.  
 DR N-PSDB; ABA93781.  
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
 PT splenic, blood or bone disorders -  
 XX  
 PS Claim 23; Page 176-177; 235pp; English.  
 XX The present invention describes a cytokine receptor designated zcytor17.  
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
 CC antineumatic, antiarthritic and muscular activities. The zcytor17  
 CC proteins are useful for treating and diagnosing lymphoid, immune,  
 CC inflammatory, splenic, blood or bone disorders. Agonists or  
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
 CC immunity and for stimulating lymphocyte proliferation, such as in the  
 CC treatment of infections involving immunosuppression, including certain  
 CC viral infections. They are also useful for inducing cytotoxicity and  
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
 CC exemplification of the present invention.  
 CC  
 XX Sequence 324 AA;  
 SQ  
 Query Match 100.0%; Score 1121; DB 23; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-103;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYAFGEKNDCTNSTSENRA 60  
 DB 20 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYAFGEKNDCTNSTSENRA 79  
 QY 61 SCSPFLPRITIPDNYTIEVEAENGQGVKSHMTYRLENIKTEPKIFRYKPVLGIKRM 120  
 DB 80 SCSPFLPRITIPDNYTIEVEAENGQGVKSHMTYRLENIKTEPKIFRYKPVLGIKRM 139  
 QY 121 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTLGLQPTTEYVI 180  
 DB 140 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTLGLQPTTEYVI 199  
 QY 181 ALRCVAVESKFSWSDMSQEKMGTEBEAP 208  
 DB 200 ALRCVAVESKFSWSDMSQEKMGTEBEAP 227

RESULT 2  
 ABB54369  
 ID ABB54369 standard; Protein; 548 AA.  
 XX ABB54369;  
 AC  
 XX 20-JAN-2003 (first entry)  
 DT  
 XX Human NR10.8 splicing variant protein SEQ ID NO:14.  
 DE  
 XX NR10; splicing variant; haematopoietin receptor; immunomodulator;  
 KW haematopoietic factor; immunological disease;  
 KW haematopoietic disease; haematopoietic cell regulation.  
 XX Homo sapiens.  
 OS  
 XX WO200277230-A1.  
 PN  
 XX 03-OCT-2002.  
 PD  
 XX 22-MAR-2002; 2002WO-JP02769.  
 PF  
 XX

PR 26-MAR-2001; 2001JP-0087298.  
 XX  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Maeda M, Yaguchi N, Hasegawa M;  
 PI  
 XX WPI; 2003-018925/01.  
 DR N-PSDB; ABQ83369.  
 PT NR10 splicing variants of hematopoietin receptor proteins and encoded  
 PT genes; applicable in searching hematopoietic factors and developing  
 PT remedies for immunological and hematopoietic diseases -  
 XX  
 PS Claim 1; Fig 19-21; 250pp; Japanese.  
 XX The present invention describes haematopoietic receptor NR10 splicing  
 CC variants (I). (I) have immunomodulator and haemostatic activities. The  
 CC proteins and encoded genes are applicable in searching for novel  
 CC haematopoietic factors, and developing remedies for immunological and  
 CC haematopoietic diseases. The haematopoietin receptor genes participate  
 CC in vivo immunomodulation and haematopoietic cell regulation, and in  
 CC the search for haematopoietic factors capable of functionally binding  
 CC to the receptors. The present sequence represents the human NR10.8  
 CC protein from the present invention.  
 CC  
 XX Sequence 548 AA;  
 SQ  
 Query Match 100.0%; Score 1121; DB 24; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-103;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYAFGEKNDCTNSTSENRA 60  
 DB 52 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYAFGEKNDCTNSTSENRA 111  
 QY 61 SCSPFLPRITIPDNYTIEVEAENGQGVKSHMTYRLENIKTEPKIFRYKPVLGIKRM 120  
 DB 112 SCSPFLPRITIPDNYTIEVEAENGQGVKSHMTYRLENIKTEPKIFRYKPVLGIKRM 171  
 QY 121 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTLGLQPTTEYVI 180  
 DB 172 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTLGLQPTTEYVI 231  
 QY 181 ALRCVAVESKFSWSDMSQEKMGTEBEAP 208  
 DB 232 ALRCVAVESKFSWSDMSQEKMGTEBEAP 259

RESULT 3  
 ABB54368  
 ID ABB54368 standard; Protein; 549 AA.  
 XX ABB54368;  
 AC  
 XX 20-JAN-2003 (first entry)  
 DT  
 XX Human NR10.7 splicing variant protein SEQ ID NO:12.  
 DE  
 XX NR10; splicing variant; haematopoietin receptor; immunomodulator;  
 KW haematopoietic factor; immunological disease;  
 KW haematopoietic disease; haematopoietic cell regulation.  
 XX Homo sapiens.  
 OS  
 XX WO200277230-A1.  
 PN  
 XX 03-OCT-2002.  
 PD  
 XX 22-MAR-2002; 2002WO-JP02769.  
 PF  
 XX 26-MAR-2001; 2001JP-0087298.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.

XX Maeda M, Yaguchi N, Hasegawa M;  
XX WPI; 2003-018925/01.  
DR N-PSDB; ABO83368.  
XX  
XX NR10 splicing variants of hematopoietin receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX  
XX Claim 1; Fig 16-18; 250pp; Japanese.  
XX  
XX The present invention describes hematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC hematopoietic factors, and developing remedies for immunological and  
CC hematopoietic diseases. The hematopoietin receptor genes participate  
CC in in vivo immunomodulation and hematopoietic cell regulation, and in  
CC the search for hematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.7.  
CC protein from the present invention.

SO Sequence 549 AA;

Query Match 100.0%; Score 1121; DB 24; Length 549;  
Best Local Similarity 100.0%; Pred. No. 5,7e-103;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 60  
DB 52 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 111  
QY 61 SCSEFLPRITIPDNYTIEVEAENGDVIKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 120  
DB 112 SCSEFLPRITIPDNYTIEVEAENGDVIKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 171  
QY 121 IOIEWIKPELAPVSSDLKTYLRFRTVNSTSMVEVNAKRNKQNTYNLTGLQPFTEYVI 180  
DB 172 IOIEWIKPELAPVSSDLKTYLRFRTVNSTSMVEVNAKRNKQNTYNLTGLQPFTEYVI 231  
QY 181 ALRCAYKESKFWSDMSQEKMGTEBEAP 208  
DB 232 ALRCAYKESKFWSDMSQEKMGTEBEAP 259

#### RESULT 4

ABP54367  
ID ABB54367 standard; Protein; 581 AA.

XX ABB54367;

XX 20-JAN-2003 (first entry)

XX Human NR10.6 splicing variant protein SEQ ID NO:10.

XX NR10; splicing variant; hematopoietin receptor; immunomodulator;  
KM haemostatic; hematopoietic factor; immunological disease;  
KM hematopoietic disease; hematopoietic cell regulation.

XX Homo sapiens.

XX WO20027230-A1.

XX 03-OCT-2002.

XX 22-MAR-2002; 2002WO-JP02769.

XX 26-MAR-2001; 2001JP-0087298.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Maeda M, Yaguchi N, Hasegawa M;  
XX

DR WPI; 2003-018925/01.  
DR N-PSDB; ABO83367.

XX NR10 splicing variants of hematopoietin receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX

XX Claim 1; Fig 13-15; 250pp; Japanese.

XX The present invention describes hematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC hematopoietic factors, and developing remedies for immunological and  
CC hematopoietic diseases. The hematopoietin receptor genes participate  
CC in in vivo immunomodulation and hematopoietic cell regulation, and in  
CC the search for hematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.6  
CC protein from the present invention.

SO Sequence 581 AA;

Query Match 100.0%; Score 1121; DB 24; Length 581;  
Best Local Similarity 100.0%; Pred. No. 6,2e-103;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 60  
DB 52 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 111  
QY 61 SCSEFLPRITIPDNYTIEVEAENGDVIKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 120  
DB 112 SCSEFLPRITIPDNYTIEVEAENGDVIKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 171  
QY 121 IOIEWIKPELAPVSSDLKTYLRFRTVNSTSMVEVNAKRNKQNTYNLTGLQPFTEYVI 180  
DB 172 IOIEWIKPELAPVSSDLKTYLRFRTVNSTSMVEVNAKRNKQNTYNLTGLQPFTEYVI 231  
QY 181 ALRCAYKESKFWSDMSQEKMGTEBEAP 208  
DB 232 ALRCAYKESKFWSDMSQEKMGTEBEAP 259

#### RESULT 5

ABB95608  
ID ABB95608 standard; Protein; 582 AA.

XX ABB95608;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO21384 SEQ ID NO: 372.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KM cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;  
KM antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23322.

XX 24-AUG-2000; 2000WO-US23328.

07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242822P.  
PR 08-NOV-2000; 2000US-070923P.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US3267P.  
PR 20-DEC-2000; 2000US-074259.  
PR 20-DEC-2000; 2000WO-US3495P.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-079649P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US0666P.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-082836P.  
PR 10-MAY-2001; 2001US-085420P.  
PR 25-MAY-2001; 2001US-085428P.  
PR 25-MAY-2001; 2001US-086034.  
PR 25-MAY-2001; 2001US-086034.  
PR 30-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.  
XX  
XX (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (FERR ) FERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODO ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLAN K J.  
PA (MARS ) MARSTERS S A.  
PA (PANU ) PAN J.  
PA (PAON ) PAONI N F.  
PA (STEP ) STEPHAN J F.  
PA (WATA ) WATANABE C K.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX MPI: 2002-171999/22.  
DR N-PSDB; ABL95746.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX Claim 11; Fig 372; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.  
XX  
XX Sequence 582 AA:  
Query Match 100.0%; Score 1121; DB 23; Length 582;  
Best Local Similarity 100.0%; Pred. No. 6.2e-103;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALPAKPNISCVYYRKNLCTWSPGKETSYYQYVRYTAPFGEKDNCTNSTSENRA 60  
Db 52 ALPAKPNISCVYYRKNLCTWSPGKETSYYQYVRYTAPFGEKDNCTNSTSENRA 111  
Qy 61 SCSPFLPRITIPDNYTIEVAENGQVYKSHMTYMLENIATKTEPPKIFVKVLGI KRM 120  
Db 112 SCSPFLPRITIPDNYTIEVAENGQVYKSHMTYMLENIATKTEPPKIFVKVLGI KRM 171  
Qy 121 IOIEWIKPELAPVSSDLKYLTRPRYVNSTSMVEVNAKRNKDNQYTNLTGLOPTEYVI 180  
Db 172 IOIEWIKPELAPVSSDLKYLTRPRYVNSTSMVEVNAKRNKDNQYTNLTGLOPTEYVI 231  
Qy 181 ALRCAYESKFSMSDSQEKMGTEBEAP 208  
Db 232 ALRCAYESKFSMSDSQEKMGTEBEAP 259  
RESULT 6  
ABB85002  
ID ABB85002 standard; Protein; 582 AA.  
XX  
AC ABB85002;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO21384 protein sequence SEQ ID NO:372.  
XX  
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.  
XX  
XX Homo sapiens.  
XX  
XX W0200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
XX 23-JUN-2000; 2000US-213637P.  
XX 20-JUL-2000; 2000US-219556P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220644P.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 02-AUG-2000; 2000US-222695P.  
XX 17-AUG-2000; 2000US-0643657.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23338.  
XX 07-SEP-2000; 2000US-230978P.  
XX 18-SEP-2000; 2000US-0664610.  
XX 18-SEP-2000; 2000US-0665350.  
XX 24-OCT-2000; 2000US-242822P.  
XX 08-NOV-2000; 2000US-070923P.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 01-DEC-2000; 2000WO-US3267P.  
XX 20-DEC-2000; 2000US-074259.  
XX 20-DEC-2000; 2000WO-US3495P.  
XX 22-JAN-2001; 2001US-0767609.  
XX 28-FEB-2001; 2001US-079649P.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-MAR-2001; 2001WO-US0666P.  
XX 09-MAR-2001; 2001US-0802706.  
XX 14-MAR-2001; 2001US-0808689.  
XX 22-MAR-2001; 2001US-0816744.  
XX 05-APR-2001; 2001US-082836P.

PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001US-0866034.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001US-0870574.  
PR 01-JUN-2001; 2001US-0870574.  
PR 01-JUN-2001; 2001US-0870574.  
XX (GERTH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
PI Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX WPI; 2002-090516/12.  
XX N-PSDB; ABL88257.  
DR  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX  
XX Claim 11; Fig 372; 565pp; English.  
XX  
XX ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to  
XX ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
XX activities, and can be used in gene therapy. The PRO polynucleotides,  
XX proteins, agonists and antagonists are useful for treating or diagnosing  
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,  
XX e.g. cardiac hypertrophy, trauma, cancer, age-related restenosis,  
XX degeneration, atherosclerosis, hypertension, arterial restenosis,  
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
XX carcinoma) and wound healing. The PRO polynucleotides have applications  
XX in molecular biology, including use as hybridisation probes, and in  
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
XX probes used in the exemplification of the present invention.  
XX  
XX  
XX Sequence 582 AA;  
XX  
XX  
XX Query Match 100.0%; Score 1121; DB 23; Length 582;  
XX Best Local Similarity 100.0%; Pred. No. 6.2e-103;  
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX  
XX 1 ALPAKPNISCVYRRKRLCTWSPGKETSQYTVKRTYAFGEKHNDCTNSTSENRA 60  
XX  
XX 52 ALPAKPNISCVYRRKRLCTWSPGKETSQYTVKRTYAFGEKHNDCTNSTSENRA 111  
XX  
XX 61 SCSEFLPRITPDVYTTVEAENGDVIKSHMTYWRLENIAKTEPPKIFRYKPVILGIKRM 120  
XX  
XX 112 SCSEFLPRITPDVYTTVEAENGDVIKSHMTYWRLENIAKTEPPKIFRYKPVILGIKRM 171  
XX  
XX 121 IQIWIKEPLAPVSSDLKYLTFRTVNSTSMWEVNAFNRKDKQYNTLGLQPTTEYVI 180  
XX  
XX 172 IQIWIKEPLAPVSSDLKYLTFRTVNSTSMWEVNAFNRKDKQYNTLGLQPTTEYVI 231  
XX  
XX 181 ALRCVAKESKFWSDMSOEKMGTEBEAP 208  
XX  
XX 232 ALRCVAKESKFWSDMSOEKMGTEBEAP 259  
XX  
XX  
XX RESULT 7  
XX AAU83637  
XX ID AAU83637 standard; Protein. 582 AA.  
XX  
XX AAU83637;  
XX AC  
XX  
XX 08-MAY-2002 (first entry)  
XX DT  
XX  
XX Human PRO protein, Seg ID No 92.  
XX DE  
XX  
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha.  
XX  
XX Homo sapiens.  
XX  
XX MO200208288-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 29-JUN-2001; 2001US-0871066.  
XX  
XX 20-JUL-2000; 2000US-219556P.  
XX 25-JUL-2000; 2000US-220585P.  
XX 25-JUL-2000; 2000US-220605P.  
XX 25-JUL-2000; 2000US-220607P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220638P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 25-JUL-2000; 2000US-220666P.  
XX 26-JUL-2000; 2000US-220893P.  
XX 28-JUL-2000; 2000US-2209710.  
XX 23-AUG-2000; 2000US-223522.  
XX 24-AUG-2000; 2000US-223328.  
XX 15-SEP-2000; 2000US-000000P.  
XX 10-NOV-2000; 2000US-0330873.  
XX 28-NOV-2000; 2000US-253646P.  
XX 01-DEC-2000; 2000US-0332678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000US-034956.  
XX 18-FEB-2001; 2001US-065620.  
XX 10-MAY-2001; 2001US-0854280.  
XX 25-MAY-2001; 2001US-0854280.  
XX  
XX (GERTH ) GENENTECH INC.  
XX  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
XX Grimaldi JC, Gurney AL, Smith V, Stephen JF, Watanabe CK, Wood WI;  
XX  
XX WPI; 2002-172001/22.  
XX N-PSDB; ABK33581.  
XX  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
XX useful for treating a PRO related disorder and for diagnosing tumours  
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
XX tumour or liver tumour -  
XX  
XX  
XX Claim 11; Figure 92; 359pp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,  
XX agonists and antagonists are useful for treating a PRO related disorder.  
XX The PRO polypeptides are useful for diagnosing tumours, especially lung  
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
XX liver tumour. The PRO polypeptides are useful for stimulating the  
XX proliferation of, or gene expression, in pericyte cells, for stimulating  
XX the proliferation or differentiation of chondrocyte cells, for  
XX stimulating the release of tumour necrosis factor-alpha from human blood,  
XX for stimulating or inhibiting the proliferation of normal human dermal  
XX fibroblast cells. The PRO polypeptide may also be used as molecular  
XX weight markers and for tissue typing. The PRO nucleic acids have  
XX applications in molecular biology, including use as hybridisation probes,  
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
XX protein sequences of the invention.  
XX  
XX  
XX Sequence 582 AA;  
XX  
XX  
XX Query Match 100.0%; Score 1121; DB 23; Length 582;  
XX Best Local Similarity 100.0%; Pred. No. 6.2e-103;  
XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX  
XX 1 ALPAKPNISCVYRRKRLCTWSPGKETSQYTVKRTYAFGEKHNDCTNSTSENRA 60

Db 52 ALPAKPENISCVYYRRKMLCTWSPGKSTSYQYVKKTYAFGEHNDCTNNSISENRA 111  
 Qy 61 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRWLENIKTEBPKEFRVKPVLGIGRM 120  
 Db 112 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRWLENIKTEBPKEFRVKPVLGIGRM 171  
 Qy 121 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVNFANRDKNQTYNLGLOPTEYVI 180  
 Db 172 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVNFANRDKNQTYNLGLOPTEYVI 231  
 Qy 181 ALRCVAKESKFWSDMSQEKMGTEBEAP 208  
 Db 232 ALRCVAKESKFWSDMSQEKMGTEBEAP 259

## RESULT 8

ABP54366  
 ID ABP54366 standard; Protein; 627 AA.

ABP54366;

20-JAN-2003 (first entry)

Human NR10.5 splicing variant protein SEQ ID NO:8.

KW NR10; splicing variant; haematopoietin receptor; immunomodulator;  
 haemostatic; haematopoietic factor; immunological disease;  
 haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

WO200272730-A1.

03-OCT-2002.

22-MAR-2002; 2002WO-JP02769.

26-MAR-2001; 2001JP-0087298.

(CHUS) CHUGAI SEIYAKU KK.

Maeda M, Yaguchi N, Hasegawa M;

WPI; 2003-018925/01.

N-PSDB; ABQ83366.

NR10 splicing variants of hematopoietin receptor proteins and encoded  
 genes, applicable in searching hematopoietic factors and developing  
 remedies for immunological and hematopoietic diseases  
 Claim 1; Fig 10-12; 250pp; Japanese.

The present invention describes haematopoietic receptor NR10 splicing  
 variants (I). (I) have immunomodulator and haemostatic activities. The  
 proteins and encoded genes are applicable in searching for novel  
 haematopoietic factors, and developing remedies for immunological and  
 haematopoietic diseases. The haematopoietin receptor genes participate  
 in in vivo immunomodulation and haematopoietic cell regulation, and in  
 the search for haematopoietic factors capable of functionally binding  
 to the receptors. The present sequence represents the human NR10.5  
 protein from the present invention.

Sequence 627 AA;

Query Match 100.0%; Score 1121; DB 24; Length 627;

Best Local Similarity 100.0%; Pred. No. 6.9e-103;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPAKPENISCVYYRRKMLCTWSPGKSTSYQYVKKTYAFGEHNDCTNNSISENRA 60  
 Db 52 ALPAKPENISCVYYRRKMLCTWSPGKSTSYQYVKKTYAFGEHNDCTNNSISENRA 111

Qy 61 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRWLENIKTEBPKEFRVKPVLGIGRM 120  
 Db 112 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRWLENIKTEBPKEFRVKPVLGIGRM 171  
 Qy 121 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVNFANRDKNQTYNLGLOPTEYVI 180  
 Db 172 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVNFANRDKNQTYNLGLOPTEYVI 231  
 Qy 181 ALRCVAKESKFWSDMSQEKMGTEBEAP 208  
 Db 232 ALRCVAKESKFWSDMSQEKMGTEBEAP 259

## RESULT 9

ABB05738  
 ID ABB05738 standard; Protein; 649 AA.

ABB05738;

01-MAY-2002 (first entry)

Human zcytor17 protein sequence SEQ ID NO:46.

KW Zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;  
 antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
 muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
 infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
 autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

WO20020721-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US20484.

26-JUN-2000; 2000US-214282P.

29-JUN-2000; 2000US-214955P.

08-FEB-2001; 2001US-267963P.

(ZYMO) ZYMOGENETICS INC.

Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;

Maurer WF;

WPI; 2002-090519/12.

N-PSDB; ABA93803.

Isolated polynucleotide encoding a cytokine receptor zcytor17 which is

useful for treating and diagnosing lymphoid, immune, inflammatory,

splenic, blood or bone disorders

Claim 18; Page 195-197; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17.  
 Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
 antirheumatic, antiarthritic and muscular activities. The zcytor17  
 proteins are useful for treating and diagnosing lymphoid, immune,  
 inflammatory, splenic, blood or bone disorders. Agonists or  
 anti-zcytor17 antibodies are useful in stimulating cell-mediated  
 immunity and for stimulating lymphocyte proliferation, such as in the  
 treatment of infections involving immunosuppression, including certain  
 viral infections. They are also useful for inducing cytotoxicity and  
 for treating leukopenias. Antagonists of zcytor17 polypeptides are useful  
 for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
 sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
 pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
 chromosome 5, specifically to the Sg11 chromosomal region. ABA93767 to  
 ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
 exemplification of the present invention.

Sequence 649 AA;  
Query Match 100.0%; Score 1121; DB 23; Length 649;  
Best Local Similarity 100.0%; Pred. No. 7, 2e-103;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSTSENRA 60  
DB 20 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSTSENRA 79  
QY 61 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYRLAKTEPPKIFRKPVLGIGKM 120  
DB 80 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYRLAKTEPPKIFRKPVLGIGKM 139  
QY 121 IQIEWIKPELAPVSSDLKTLRFTVNSTSMVEVNAKRNKQNTNLTGLQPFTEYVI 180  
DB 140 IQIEWIKPELAPVSSDLKTLRFTVNSTSMVEVNAKRNKQNTNLTGLQPFTEYVI 199  
QY 181 ALRCAYESKFSWSDMSQEKMGTEEBAP 208  
DB 200 ALRCAYESKFSWSDMSQEKMGTEEBAP 227

RESULT 10  
AAB51242  
ID AAB51242 standard; Protein; 652 AA.

AC AAB51242;  
XX  
XX  
DT 26-MAR-2001 (first entry)  
DE Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.

XX Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;  
KW immunoregulation; haematopoietic cell regulation; transmembrane;  
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;  
KW metal allergy; pollen allergy.  
XX Homo sapiens.

XX W02000425314-A1.  
XX 14-DEC-2000.

XX 01-JUN-2000; 2000WO-JP03556.

XX 02-JUN-1999; 99JP-0155797.  
XX 30-JUL-1999; 99JP-0217797.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Maeda M, Yaguchi N;

XX WPI; 2001-061720/07.

XX N-PSDB; AAC92337.

PT Hematopoietin receptor protein NR10 for screening potential ligands for  
PT treatment of immune and haematopoietic disorders such as autoimmune  
PT diseases and allergies -

XX Claim 1; Fig 3-5; 127pp; Japanese.

XX The present sequence represents a human haemopoietin receptor protein  
XX (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane  
XX protein and a soluble protein. NR10 is a haemopoietin receptor molecule  
XX which participates in immunoregulation and haematopoietic cell  
XX regulation in vivo, and is useful in searching for haematopoietic  
XX factors capable of binding to the receptor. NR10 can be used for the  
XX identification of substances for the treatment and prevention of immune  
XX and haematopoietic disorders including autoimmune diseases and allergies  
XX such as metal and pollen allergy.

XX Sequence 652 AA;

Query Match 100.0%; Score 1121; DB 22; Length 652;  
Best Local Similarity 100.0%; Pred. No. 7, 3e-103;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSTSENRA 60  
DB 33 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSTSENRA 92  
QY 61 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYRLAKTEPPKIFRKPVLGIGKM 120  
DB 93 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYRLAKTEPPKIFRKPVLGIGKM 152  
QY 121 IQIEWIKPELAPVSSDLKTLRFTVNSTSMVEVNAKRNKQNTNLTGLQPFTEYVI 180  
DB 153 IQIEWIKPELAPVSSDLKTLRFTVNSTSMVEVNAKRNKQNTNLTGLQPFTEYVI 212  
QY 181 ALRCAYESKFSWSDMSQEKMGTEEBAP 208  
DB 213 ALRCAYESKFSWSDMSQEKMGTEEBAP 240

RESULT 11  
AAB24028  
ID AAB24028 standard; Protein; 652 AA.

AC AAB24028;  
XX  
XX  
DT 23-SEP-2002 (first entry)  
DE Human HPR1 variant protein #2.

XX Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;  
KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
KW osteoclast disorder; periodontitis; acute polymyoneuropathy; Bell's palsy;  
KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
KW ischaemic disease; variant.

XX Homo sapiens.

XX W0200229060-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US31634.

XX 06-OCT-2000; 2000US-238706P.

XX 13-OCT-2000; 2000US-240476P.

XX 20-FEB-2001; 2001US-270282P.

XX (IMNV) IMMUNEX CORP.

XX Cosman DJ, Mosley BA, Bird TA, Dubose RF, Willey SR;

XX WPI; 2002-330172/36.

PT Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,  
PT useful for treating cell proliferation, metabolic, and reproductive  
PT hormone related conditions -

XX Disclosure; Page 110-112; 136pp; English.

XX The present invention relates to human and murine haematopoietin receptor  
XX polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
XX treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
XX anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
XX resulting from a lack of bone-forming cells. They are also useful for

treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematological and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelodysplastic syndromes (including refractory anaemia, refractory anaemia with ringed sideroblasts or with excess blasts), idiopathic thrombocytopenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, peridontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence is human HPR1 variant protein.

XX XX Sequence 652 AA;

Query Match 100.0%; Score 1121; DB 23; Length 652;  
Best Local Similarity 100.0%; Pred. No. 7.3e-103;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 60  
DB 33 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 92  
QY 61 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEPPKIFRYKPVLGIRKM 120  
DB 93 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEPPKIFRYKPVLGIRKM 152  
QY 121 IQIEWIKPELAPVSSDLKTYTLRFTVNSTSWMEVFAKNRDKXQNTYNLGLQPTTEYVI 180  
DB 153 IQIEWIKPELAPVSSDLKTYTLRFTVNSTSWMEVFAKNRDKXQNTYNLGLQPTTEYVI 212  
QY 181 ALRCVAKSKFWSQSKMGTEBEAP 208  
DB 213 ALRCVAKSKFWSQSKMGTEBEAP 240

RESULT 12

AAB51244  
ID AAB51244 standard; Protein; 662 AA.

XX AC AAB51244;

XX DT 26-MAR-2001 (first entry)

XX DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.

XX XX Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;

KW immunoregulation; haematopoietic cell regulation; transmembrane;

KM immune disorder; haematopoietic disorder; autoimmune disease; allergy;

XX KM metal allergy; pollen allergy.

XX OS Homo sapiens.

XX PN WO200075314-A1.

XX PD 14-DEC-2000.

XX PF 01-JUN-2000; 2000WO-JP03556.

XX PR 02-JUN-1999; 99JP-0155797.

XX PR 30-JUN-1999; 99JP-0217797.

XX XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Maeda M, Yaguchi N;

XX WP1; 2001-061720/07.

DR N-PSDB; AAC923350.

PT Hematopoietin receptor protein NR10 for screening potential ligands for treatment of immune and hematopoietic disorders such as autoimmune diseases and allergies -

XX Claim 1; Fig 13-14; 127pp; Japanese.

XX XX The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and pollen allergy.

XX XX Sequence 662 AA;

Query Match 100.0%; Score 1121; DB 22; Length 662;  
Best Local Similarity 100.0%; Pred. No. 7.5e-103;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 60  
DB 33 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 92  
QY 61 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEPPKIFRYKPVLGIRKM 120  
DB 93 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEPPKIFRYKPVLGIRKM 152  
QY 121 IQIEWIKPELAPVSSDLKTYTLRFTVNSTSWMEVFAKNRDKXQNTYNLGLQPTTEYVI 180  
DB 153 IQIEWIKPELAPVSSDLKTYTLRFTVNSTSWMEVFAKNRDKXQNTYNLGLQPTTEYVI 212  
QY 181 ALRCVAKSKFWSQSKMGTEBEAP 208  
DB 213 ALRCVAKSKFWSQSKMGTEBEAP 240

RESULT 13

AAE24029  
ID AAE24029 standard; Protein; 662 AA.

XX AC AAE24029;

XX DT 23-SEP-2002 (first entry)

XX DE Human HPR1 variant protein #3.

XX XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;

KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;

KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;

KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;

KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;

KW osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;

KM anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;

KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;

KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;

KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;

KM ischaemic disease; variant.

XX OS Homo sapiens.

XX NO200229060-A2.  
 PN 11-APR-2002.  
 PD 05-OCT-2001; 2001WO-US31634.  
 PF 06-OCT-2000; 2000US-238706P.  
 PR 13-OCT-2000; 2000US-240476P.  
 PR 20-FEB-2001; 2001US-270282P.  
 XX (IMMV ) IMMUNEX CORP.  
 PA Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,  
 PI WPI; 2002-330172/36.  
 DR Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 PT hormone related conditions -  
 PS Disclosure; Page 112-115; 136pp; English.  
 XX The present invention relates to human and murine haematopoietin receptor  
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukaemia and tumour  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related conditions. They are useful for treating various haematologic and  
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (NSCLC and SCLC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such  
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC myasthenia gravis, chronic neuronal degeneration, stroke including  
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful  
 CC for treating various other disorders such as osteoporosis, obesity,  
 CC deficient mammary development and infertility. The present sequence  
 CC is human HPR1 variant protein.  
 XX  
 SQ Sequence 662 AA;  
 Query Match 100.0%; Score 1121; DB 23; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-103; Indels 0; Gaps 0;  
 Matches 208; Conservative 0; Mismatches 0;  
 QY 1 ALPAKPNISCVYYRKNLTCTWSPGKETSYYQYTVKRYTAFGEKHDNCTNSTSENRA 60  
 DB 33 ALPAKPNISCVYYRKNLTCTWSPGKETSYYQYTVKRYTAFGEKHDNCTNSTSENRA 92  
 QY 61 SCSEFFLRITIPDNTTIEVAENGQVYKSHMTYRLNLTAKTEPPKIFVYKPVLAGIKRM 120  
 DB 93 SCSEFFLRITIPDNTTIEVAENGQVYKSHMTYRLNLTAKTEPPKIFVYKPVLAGIKRM 152  
 QY 121 IOIEWIKPELAPVSSDKYTLRFTVNSTSMENYFNPAKRNKQKQYTNLTGLQPFITYVI 180  
 DB 153 IOIEWIKPELAPVSSDKYTLRFTVNSTSMENYFNPAKRNKQKQYTNLTGLQPFITYVI 212

QY 181 ALRCAYESKFWSDWSEKMGTEBEAP 208  
 DB 213 ALRCAYESKFWSDWSEKMGTEBEAP 240  
 RESULT 14  
 ABB05741  
 ID ABB05741 standard; Protein; 662 AA.  
 AC ABB05741;  
 XX 01-MAY-2002 (first entry)  
 DT Human zcytor17 protein sequence SEQ ID NO:54.  
 DE  
 XX Zcytor17, chromosome 5; 5q11, cytokine receptor; immunomodulatory;  
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cyostatic;  
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.  
 XX Homo sapiens.  
 OS  
 XX WO200200721-A2.  
 PN 03-JUN-2002.  
 PD 26-JUN-2001; 2001WO-US20484.  
 PF 26-JUN-2000; 2000US-214282P.  
 XX 29-JUN-2000; 2000US-214955P.  
 PR 08-FEB-2001; 2001US-267963P.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL,  
 PI Maurer WF;  
 PI WPI; 2002-090519/12.  
 DR N-PSDB; ABA93808.  
 DR Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
 PT splenic, blood or bone disorders -  
 PS Example 1; Page 204-206; 235pp; English.  
 XX The present invention describes a cytokine receptor designated zcytor17.  
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,  
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17  
 CC proteins are useful for treating and diagnosing lymphoid, immune,  
 CC inflammatory, splenic, blood or bone disorders. Agonists or  
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
 CC immunity and for stimulating lymphocyte proliferation, such as in the  
 CC treatment of infections involving immunosuppression, including certain  
 CC viral infections. They are also useful for inducing cytotoxicity and  
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 662 AA;  
 Query Match 100.0%; Score 1121; DB 23; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-103; Indels 0; Gaps 0;  
 Matches 208; Conservative 0; Mismatches 0;  
 QY 1 ALPAKPNISCVYYRKNLTCTWSPGKETSYYQYTVKRYTAFGEKHDNCTNSTSENRA 60

Db 33 ALPAKPENISCVYYRRKULCTWSPGKETSQTQVTKRTYAFGEKHDNCTNNSSTSENRA 92  
QY 61 SCSFPLPRITIPDNYTIEVEANGDGVKSHMTYWRLENIAKTEPPKIFRVKVLGIGKM 120  
Db 93 SCSFPLPRITIPDNYTIEVEANGDGVKSHMTYWRLENIAKTEPPKIFRVKVLGIGKM 152  
QY 121 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRKKDKQTYNLTLGLOPFTTEYVI 180  
Db 153 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRKKDKQTYNLTLGLOPFTTEYVI 212  
QY 181 ALRCAVSKSKFWSMDMSOEKMGMTBEEAP 208  
Db 213 ALRCAVSKSKFWSMDMSOEKMGMTBEEAP 240

RESULT 15  
ABP54363  
ID ABP54363 standard; Protein; 681 AA.

XX AC ABP54363;

DT 20-JAN-2003 (first entry)

DE Human NR10.3 splicing variant protein SEQ ID NO:2.

XX NR10; splicing variant; haematopoietic receptor; immunomodulator;

KM haemostatic; haematopoietic factor; immunological disease;

XX haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

FN WO200277230-A1.

PD 03-OCT-2002.

PP 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Maeda M, Yaguchi N, Hasegawa M;

DR WPI; 2003-018925/01.

DR N-PSDB; ABQ83363.

XX NR10 splicing variants of hematopoietic receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX

PS Example 2; Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors, and developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietic receptor genes participate  
CC in in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.3  
CC protein from the present invention.

XX Sequence 681 AA;

QY Query Match 100.0%; Score 1121; DB 24; Length 681;

Best Local Similarity 100.0%; Pred. No. 7.8e-103;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPENISCVYYRRKULCTWSPGKETSQTQVTKRTYAFGEKHDNCTNNSSTSENRA 60  
52 ALPAKPENISCVYYRRKULCTWSPGKETSQTQVTKRTYAFGEKHDNCTNNSSTSENRA 111

QY 61 SCSFPLPRITIPDNYTIEVEANGDGVKSHMTYWRLENIAKTEPPKIFRVKVLGIGKM 120  
Db 112 SCSFPLPRITIPDNYTIEVEANGDGVKSHMTYWRLENIAKTEPPKIFRVKVLGIGKM 171  
QY 121 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRKKDKQTYNLTLGLOPFTTEYVI 180  
Db 172 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRKKDKQTYNLTLGLOPFTTEYVI 231  
QY 181 ALRCAVSKSKFWSMDMSOEKMGMTBEEAP 208  
Db 232 ALRCAVSKSKFWSMDMSOEKMGMTBEEAP 259

Search completed: August 18, 2003, 13:27:00  
Job time : 80.0499 secs

Page 1

td.

March time 25.6912 Seconds  
(without alignments)  
...555 Million cell updates/sec

..SKFWS DWSQEKMGMTBEAP 208

ers: 328717

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DMB.pep:\*  
DMB.pep:\*  
DMB.pep:\*  
S.COMB.pep:\*  
files1.pep.\*

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of the result being printed,  
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| Description |                  |
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| 9           | Sequence 5, App  |
| 8           | Sequence 5, App  |
| 7           | Sequence 5, App  |
| 6           | Sequence 5, App  |
| 5           | Sequence 5, App  |
| 4           | Sequence 5, App  |
| 3           | Sequence 5, App  |
| 2           | Sequence 5, App  |
| 1           | Sequence 5, App  |
| 0           | Sequence 5, App  |
| 29          | Sequence 29, App |
| 28          | Sequence 24, App |
| 27          | Sequence 26, App |
| 26          | Sequence 26, App |
| 25          | Sequence 26, App |
| 24          | Sequence 24, App |
| 23          | Sequence 24, App |
| 22          | Sequence 24, App |
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| 16          | Sequence 24, App |
| 15          | Sequence 24, App |
| 14          | Sequence 24, App |
| 13          | Sequence 24, App |
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| 3           | Sequence 24, App |
| 2           | Sequence 24, App |
| 1           | Sequence 24, App |
| 0           | Sequence 24, App |

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| Sequence 20, | Appb   |
| Sequence 17, | Appb   |
| Sequence 22, | Appb   |
| Sequence 25, | Appb   |
| Sequence 18, | Appb   |
| Sequence 2,  | Appb.1 |
| Sequence 4,  | Appb.1 |
| Sequence 21, | Appb   |
| Sequence 23, | Appb   |
| Sequence 27, | Appb   |
| Sequence 28, | Appb   |
| Sequence 31, | Appb   |
| Sequence 19, | Appb   |
| Sequence 30, | Appb   |
| Sequence 2,  | Appb.1 |
| Sequence 6,  | Appb.1 |
| Sequence 5,  | Appb.1 |

942

942

942

858

ersion 3.0

[illegible]

APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT  
MODULATE BODY WEIGHT USING THE OB RECEPTOR  
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,455B  
FILING DATE: 22-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-599-455B-5

Query Match 24.0%; Score 268.5; DB 2; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5.7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKENISCVYYRKNLITWSPKETS-TOYTK---RTYAFGE---KHD---NCTN 52  
DB 97 PEKKNISCVYYRKNLITWSPKETS-TOYTK---RTYAFGE---KHD---NCTN 52  
QY 53 SSTEENRASCFLPRITPDNYTIEVAENGGVKS-HMTYWRLENIATPEPKIFRV 111  
DB 157 YST-----YFV-----NIEWWEAENALGKVTSDHINPDYKV-KPNPPLSLV 201  
QY 112 KPVLGIRKMIQIEMIKPELAPVSSDLKTLRFRVNSTSMWEVNFAPKRRKDKQNTYULG 171  
DB 202 INSEELSSILKLTWTNPSIKSVII-LKYNIQRTKASTWSQIP-PEDTASTRSSFTVOD 259  
QY 172 LQPTFVYIALRCVAKESK-FWSDMSORHMGMTTEEAR 208  
DB 260 LKPTFVYIRICMEKDGKGYSDMSEASGITTEDRP 297

RESULT 3  
US-09-069-781B-5  
Sequence 5, Application US/09069781B  
Patent No. 6287782  
GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
INCLUDING OBESITY AND CACHEXIA  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,781B  
FILING DATE: 29-APRIL-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/864,564  
FILING DATE: 28-MAY-1997  
APPLICATION NUMBER: US 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: US 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: US 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: US 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: US 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: US 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: US 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: US 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/082001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-069-781B-5

Query Match 24.0%; Score 268.5; DB 3; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5.7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKENISCVYYRKNLITWSPKETS-TOYTK---RTYAFGE---KHD---NCTN 52  
DB 97 PEKKNISCVYYRKNLITWSPKETS-TOYTK---RTYAFGE---KHD---NCTN 52  
QY 53 SSTEENRASCFLPRITPDNYTIEVAENGGVKS-HMTYWRLENIATPEPKIFRV 111  
DB 157 YST-----YFV-----NIEWWEAENALGKVTSDHINPDYKV-KPNPPLSLV 201  
QY 112 KPVLGIRKMIQIEMIKPELAPVSSDLKTLRFRVNSTSMWEVNFAPKRRKDKQNTYULG 171  
DB 202 INSEELSSILKLTWTNPSIKSVII-LKYNIQRTKASTWSQIP-PEDTASTRSSFTVOD 259

Qy 172 LQPTFVYIALRCAYKESK-FWSDWSQKMGTEEBAP 208  
Db 260 LKPFTEYVFRIRCKMEDGKGYSDWSEBASGITVEDRP 297

RESULT 4

US-09-137-132-5  
Sequence 5, Application US/09137132  
Patent No. 6380363  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/137,132  
FILING DATE: 18-AUG-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/864,564  
FILING DATE: 28-MAY-1997  
APPLICATION NUMBER: 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-137-132-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5.7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

Qy 3 PAKPENISCVYYRRKNTCTSPKETS-YQYVTK---RTYAGE---KHD---NCTTN 52  
Db 97 PEKPNLSICIVNEGKRCMECDGREGTHLETNFTLKSMAWTHKFAKCRKADPTPTCTVD 156  
Qy 53 STSENRRASCSEFLPRITIPPNYTLVEAENDGVYKS-HNTYMWLENIATKEPEKIRV 111  
Db 157 YST-----YFV-----NIEVWEAENALGKVTSDHINFDVYRV-KENPHNLISV 201  
Qy 112 KVLGKIMIQLEWIKPELAPVSDLYTLRFRYVNSTSWMEVNFARKKDKQNTYNLTG 171  
Db 202 INSELSLILKTLWTNPISIKSVII-LKYNIQRTDASTWGIIP-PEDTASTRSSFTYQD 259  
Qy 172 LQPTFVYIALRCAYKESK-FWSDWSQKMGTEEBAP 208  
Db 260 LKPFTEYVFRIRCKMEDGKGYSDWSEBASGITVEDRP 297

RESULT 5

US-08-864-564A-5  
Sequence 5, Application US/08864564A  
Patent No. 6395498  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,564A  
FILING DATE: 28-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids

TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-864-564A-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5,7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKULCTWSPGKESY--TOYTK---RTYAFGE---KHD---NCTTN 52  
DB 97 PEKPNLSCTIVNEGKMRCEMDGGRHLETFILKSEWATHKPADCKAKRDTPTSTVD 156  
DB 157 YST-----VYFV-----NIEWVEAENALGKVTSDHINPDYKVK-KPNPNLSV 201  
QY 112 KPVLGIRKMIQIEMIKELAPVSSDLKTLRFTVNSTSMVEVNFANRKNQTYNLG 171  
DB 202 INSEELSSILKLTWNTNPSIKSVII-LKYNIQYRTKQDASTWSQIP-PEDTASTRSSFTVOD 259  
QY 172 LOPTEYVIALRCVAKESK-FMSDMSOEKGMTEEAR 208  
DB 260 LKPFTEYVRIRCKEDGKGYMSDMSSEASGITIEDRP 297

## RESULT 6

US-09-094-410-5  
Sequence 5, Application US/09094410  
Patent No. 6403552

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,410

FILING DATE: 09-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-094-410-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5,7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKULCTWSPGKESY--TOYTK---RTYAFGE---KHD---NCTTN 52  
DB 97 PEKPNLSCTIVNEGKMRCEMDGGRHLETFILKSEWATHKPADCKAKRDTPTSTVD 156  
DB 157 YST-----VYFV-----NIEWVEAENALGKVTSDHINPDYKVK-KPNPNLSV 201  
QY 112 KPVLGIRKMIQIEMIKELAPVSSDLKTLRFTVNSTSMVEVNFANRKNQTYNLG 171  
DB 202 INSEELSSILKLTWNTNPSIKSVII-LKYNIQYRTKQDASTWSQIP-PEDTASTRSSFTVOD 259  
QY 172 LOPTEYVIALRCVAKESK-FMSDMSOEKGMTEEAR 208  
DB 260 LKPFTEYVRIRCKEDGKGYMSDMSSEASGITIEDRP 297

## RESULT 7

US-08-708-123D-5  
Sequence 5, Application US/08708123D  
Patent No. 6482927

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/708,123D

FILING DATE: 03-SEP-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-708-123D-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5.7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKRLTCTWSPGKETS-TOYTK---RTAFGE---KHD---NCTTN 52  
DB 97 PEKPKLSCITVNEGKKRCWEGRETHLETFTLSKSWATHKFAOCKARDDPTSCYD 156  
QY 53 SSTSENARSCSFFLPITIPDNYTIEVEANGDGVKS-HMTYWRLENIAKTEPPKIFRY 111  
DB 157 YST-----VFV-----NIEWVEANLGGKTSIDHINDPYKY-KRPNHLSV 201  
QY 112 KPVLGKRMQIEMIKELAPVSSDKYTLRFRYVNSTSMVEVFNKRNKQNTNLTG 171  
DB 202 INSEELSIILKLTWTPSISKSVII-LKYNIQRTKQASTWSQIP-PEDTASTRSSPTVOD 259  
QY 172 LQPTFEYVIALCAVKEK-FWSDWSEKMGTEEAP 208  
DB 260 LKPFTEYVFRIRCKEDGKGWSDWSEASGITVEDRP 297

## RESULT 8

US-08-583-153A-5  
Sequence 5, Application US/08583153A  
Patent No. 6506877  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Cuiper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
TITLE OF INVENTION: OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153A  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/016001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-583-153A-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;  
Best Local Similarity 30.3%; Pred. No. 5.7e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKRLTCTWSPGKETS-TOYTK---RTAFGE---KHD---NCTTN 52  
DB 97 PEKPKLSCITVNEGKKRCWEGRETHLETFTLSKSWATHKFAOCKARDDPTSCYD 156  
QY 53 SSTSENARSCSFFLPITIPDNYTIEVEANGDGVKS-HMTYWRLENIAKTEPPKIFRY 111  
DB 157 YST-----VFV-----NIEWVEANLGGKTSIDHINDPYKY-KRPNHLSV 201  
QY 112 KPVLGKRMQIEMIKELAPVSSDKYTLRFRYVNSTSMVEVFNKRNKQNTNLTG 171  
DB 202 INSEELSIILKLTWTPSISKSVII-LKYNIQRTKQASTWSQIP-PEDTASTRSSPTVOD 259  
QY 172 LQPTFEYVIALCAVKEK-FWSDWSEKMGTEEAP 208  
DB 260 LKPFTEYVFRIRCKEDGKGWSDWSEASGITVEDRP 297

## RESULT 9

US-08-638-524B-5  
Sequence 5, Application US/08638524B  
Patent No. 6548269  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Cuiper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
TITLE OF INVENTION: CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/638,524B  
FILING DATE: 26-APR-1996  
PRIOR APPLICATION DATA:

```

      FILING DATE: 19-MAR-1997
      CLASSIFICATION: 536
      ATTORNEY/AGENT INFORMATION:
        NAME: ESMOND, ROBERT W.
        REGISTRATION NUMBER: 32,893
        REFERENCE/DOCKET NUMBER: 0623.0530001
        TELECOMMUNICATION INFORMATION:
          TELEPHONE: (202)371-2600
          TELEFAX: (202)371-2540
        INFORMATION FOR SEQ ID NO: 4:
          SEQUENCE CHARACTERISTICS:
            LENGTH: 658 amino acids
            TYPE: amino acid
            TOPOLOGY: linear
          MOLECULE TYPE: protein
          US-08-825-558-4

Query Match      24.0%; Score 268.5; DB 2; Length 658;
Best Local Similarity 30.3%; Pred. No. 8,88-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11

QY      3 PAKENISCVYYRYKRLCTWSPGKETS-Y-TQYTVK--RTYAGE--KHD--NCTTN 52
DB      126 PEKRNKSLCTINEGKKORCEWDGGRETHLENTFLTKSEWATHKPKADDTPTSCVD 185
QY      53 SSTSENKASCSFPLRPTIPDNTITIEVAENGQVYKS-HMTYRLENIATPEPKIRY 111
DB      186 YST-----YFPV-----NEWWEAEVALGKVTSDHINFPYKCV-KNPPHNLV 230
QY      112 KPVGLGRMIQIEIKPELAPVSSDLKYTLRFRTVNTSWMEVFAKRNKDKQNTYLTG 171
DB      231 INSELSELILKLTWTNDSIKSVII-LKYNIQYRTKDSYMSQIP-PEDTASTRSSFTYQD 288
QY      172 LQPFTEYVIALRCAYKESK-FWSDWSQEKMGMTKEEAP 208
DB      289 LKPFTEYVPIRCKEKDGKGYDWSDEASGITYEDRP 326

RESULT 11
US-09-312-611-4
: Sequence 4, Application US/09312611
: Patent No. 6380160
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/312,611
: FILING DATE: 17-MAY-1999
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: ESMOND, ROBERT W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0623.0530002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:

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; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-312-611-4

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|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 24.0%;           | Score 268.5;       | DB 4;      | Length 658; |
| Best Local Similarity | 30.3%;           | Pred. No. 8.8e-21; |            |             |
| Matches 66;           | Conservative 47; | Mismatches 76;     | Indels 29; | Gaps 11;    |

[illegible]

RESULT 12  
US-07-797-556-2

; Sequence 2, Application US/07797556  
; Patent No. 5262522

GENERAL INFORMATION:  
APPLICANT: Gearing, David P.  
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia  
TITLE OF INVENTION: Inhibitory Factor  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle

STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.22  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/797,556  
FILING DATE: 19911122

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2607  
TELECOMMUNICATION INFORMATION:

```

? TELEPHONE: 206-587-0430
? TELEFAX: 206-567-0606
? INFORMATION FOR SEQ ID NO: 2
? SEQUENCE CHARACTERISTICS:
? LENGTH: 708 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-07-797-556-2

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|                       |           |   |         |                    |
|-----------------------|-----------|---|---------|--------------------|
| Query Match           | 24.0%     | Score 268.5   | DB 1    | Length 708         |
| Best Local Similarity | 30.3%     | Pred. No.   | 9.8e-21 |                    |
| Matches               | 66        | Conservative  | 47      | Indels 29; Gaps 11 |
| Oy                    | 3         | PAKPENISCVYYRYRNILCTWSPGKETSY--QYTVK-----RTAFPE---KHD---NCTTN | 52      |                    |
|                       | :   :   : | :           :   :   | :       | :     :            |

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Db      128 PEKPKNLSCIIVNEBKXKREMDGCGRETHLEINFLILKSMWAIHKADCKARDPITSCIVD 165
Qy      53 SSTSENRRASCSEFLPRITIPDNYITTEVAENGDVIKS-HMTYRLNIAKTEBPKIFRY 111
      186 YST-----VYFV-----NIEVVAENALGKVTSDHINFDPPYKV-KPNPPNLSV 230
Qy      112 KPVLTGKRMIOIEMWKPELAPVSSDLKTYLTPRVYNTSGMSEVNFAPAKRKDKNOTYLTG 171
Db      231 INSEBELSILKLTWNPISIKSVIL-LKNIOIYRTDASWQSQIP-PEDTASTSSFTVOD 288
Qy      172 LQFTEYVALACAVKESK-FWSDSOEKMGMTTEBP 208
Db      289 LKPFTEYFRICKMEKDGKYSWDSSEASGITYEDRP 326

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RESULT 13

US-06-508-081-2  
; Sequence 2, Application US/08308881  
; Patent No. 5783672

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?
?
?      ZIP: 98101
?
?      COMPUTER READABLE FORM:
?
?      MEDIUM TYPE: Floppy disk
?
?      COMPUTER: Apple Macintosh
?
?      OPERATING SYSTEM: Apple 7.1
?
?      SOFTWARE: Microsoft Word, Version 5.1a
?
?      CURRENT APPLICATION DATA:
?
?      APPLICATION NUMBER: US/08/308,881
?
?      FILING DATE: 12-SEP-1994
?
?      CLASSIFICATION: 435
?
?      PRIOR APPLICATION DATA:

```

1 APPLICATION NUMBER: US 08/249,555  
2 FILING DATE: 26-MAY-1994  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Seese, Kathryn A.  
5 REGISTRATION NUMBER: 32,172  
6 REFERENCE/DOCKET NUMBER: 2614-A  
7 TELECOMMUNICATION INFORMATION:  
8 TELEPHONE: (206) 587-0430  
9 TELEFAX: (206) 233-0644  
0 TELEXT: 756822

```

; INFORMATION FOR SEQ ID NO: 2
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 708 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein

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US-08-308-981-2
Query Match      24.0%; Score 268.5; DB 1; Length 708;
Best Local Similarity 30.3%; Pred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11

QY      3 PAKENISGVYYRRKRLCTWSPGKEIYSV-IQYIYK---RIVARGE---KHD---NQTIN 52
       |||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      126 PEKPKNLCSTIVNEGKKMRCEMDGGRETHLENTFLTKSEMAVHKPADCAKDPTSCITVD 165
               ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      53 SSTSENRAACSFPLPRITIPDNYITVEVAENGDDVIKS-HHTYKRLENIAKTEPPKIFRY 111
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      186 YST-----VFV-----NIEVWAENAALGKVTSDHINFPPVKV-KPNPPHNLVS 230
               ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      112 KPVIGIKRMIOEWIKPELAPVSDLKTTLAFRYTNSSMWEUVFAQRDRDKQTYNLUG 171
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db 231 INSEELSLIKLWTWNPISKVIIL-KYNIQYRTKDSWISQIP-PEDTASTRSSFTVOD 288  
QY 172 LQPFTEYVIALRCAYKESK-FWSDMSQEKMGMTSEAP 208  
Db 289 LKPFTEYVIRIRCKMEDGKGWSDMSBESASGITVEDRP 326

RESULT 14  
US-09-058-263-2  
Sequence 2, Application US/09058263  
Patent No. 5891997

GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/058,263  
FILING DATE:  
CLASSIFICATION:  
Prior Application Number:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 708 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-058-263-2

Query Match 24.0%; Score 268.5; DB 2; Length 708;  
Best Local Similarity 30.3%; Pred. No. 9.8e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYIRKRLCTWSPGKETS-TOYTVK---RTYAFGE---KHD---NCTTN 52  
Db 126 PEKPKNLSCIVNEGKKRCCEWGDGRTHLETNFTLSEWATHKFAACKAKRDPPTSCTVD 185  
QY 53 SSTSENBRASCSEFLPRITIPDNNTIIEVEANGDGVKS-HMTYWRLENIATKEPPKIFRY 111  
Db 186 YST-----YTV-----NIEWVEAENALGKVTSDHINDPYKY-KNPFNLSV 230  
QY 112 KPVLGIRKMIQIEMIKPELAPVSSDKYTLRFRVNSTSMVEVNAKRNKQNTYNTLG 171  
Db 231 INSEELSLIKLWTWNPISKVIIL-KYNIQYRTKDSWISQIP-PEDTASTRSSFTVOD 288  
QY 172 LQPFTEYVIALRCAYKESK-FWSDMSQEKMGMTSEAP 208  
Db 289 LKPFTEYVIRIRCKMEDGKGWSDMSBESASGITVEDRP 326

RESULT 15  
US-09-059-099-2

Sequence 2, Application US/09059099  
Patent No. 5925740

GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/059,099  
FILING DATE:  
CLASSIFICATION:  
Prior Application Number:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 708 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-059-099-2

Query Match 24.0%; Score 268.5; DB 2; Length 708;  
Best Local Similarity 30.3%; Pred. No. 9.8e-21;  
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYIRKRLCTWSPGKETS-TOYTVK---RTYAFGE---KHD---NCTTN 52  
Db 126 PEKPKNLSCIVNEGKKRCCEWGDGRTHLETNFTLSEWATHKFAACKAKRDPPTSCTVD 185  
QY 53 SSTSENBRASCSEFLPRITIPDNNTIIEVEANGDGVKS-HMTYWRLENIATKEPPKIFRY 111  
Db 186 YST-----YTV-----NIEWVEAENALGKVTSDHINDPYKY-KNPFNLSV 230  
QY 112 KPVLGIRKMIQIEMIKPELAPVSSDKYTLRFRVNSTSMVEVNAKRNKQNTYNTLG 171  
Db 231 INSEELSLIKLWTWNPISKVIIL-KYNIQYRTKDSWISQIP-PEDTASTRSSFTVOD 288  
QY 172 LQPFTEYVIALRCAYKESK-FWSDMSQEKMGMTSEAP 208  
Db 289 LKPFTEYVIRIRCKMEDGKGWSDMSBESASGITVEDRP 326

Search completed: August 18, 2003, 13:32:20  
Job time: 26.6912 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: August 18, 2003, 13:27:13 ; Search time 27.1734 Seconds  
(without alignments)  
1002.770 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_20\_227

Perfect score: 1121  
Sequence: 1 ALPAPENISCVYRKXLT.....SKFWSDSQEKMGTEBEAP 208

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID                    | Description       |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1          | 1121  | 100.0       | 324    | 11 US-09-892-949-18   | Sequence 18, Appl |
| 2          | 1121  | 100.0       | 582    | 12 US-10-216-163-92   | Sequence 92, Appl |
| 3          | 1121  | 100.0       | 582    | 15 US-10-227-884-92   | Sequence 92, Appl |
| 4          | 1121  | 100.0       | 582    | 15 US-10-230-163-92   | Sequence 92, Appl |
| 5          | 1121  | 100.0       | 582    | 15 US-10-230-338-92   | Sequence 92, Appl |
| 6          | 1121  | 100.0       | 582    | 15 US-10-218-631-92   | Sequence 92, Appl |
| 7          | 1121  | 100.0       | 582    | 15 US-10-230-414-92   | Sequence 92, Appl |
| 8          | 1121  | 100.0       | 582    | 15 US-10-216-1159A-92 | Sequence 92, Appl |
| 9          | 1121  | 100.0       | 582    | 15 US-10-218-849-92   | Sequence 92, Appl |
| 10         | 1121  | 100.0       | 582    | 15 US-10-227-873-92   | Sequence 92, Appl |
| 11         | 1121  | 100.0       | 582    | 15 US-10-227-883-92   | Sequence 92, Appl |
| 12         | 1121  | 100.0       | 582    | 15 US-10-219-076-92   | Sequence 92, Appl |
| 13         | 1121  | 100.0       | 582    | 15 US-10-230-434-92   | Sequence 92, Appl |
| 14         | 1121  | 100.0       | 582    | 15 US-10-219-003-92   | Sequence 92, Appl |
| 15         | 1121  | 100.0       | 582    | 15 US-10-219-075-92   | Sequence 92, Appl |

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| 16 | 1121 | 100.0 | 582 | 15 US-10-219-464-92  | Sequence 92, Appl |
| 17 | 1121 | 100.0 | 582 | 15 US-10-219-466-92  | Sequence 92, Appl |
| 18 | 1121 | 100.0 | 582 | 15 US-10-219-479-92  | Sequence 92, Appl |
| 19 | 1121 | 100.0 | 582 | 15 US-10-219-481-92  | Sequence 92, Appl |
| 20 | 1121 | 100.0 | 582 | 15 US-10-230-260-92  | Sequence 92, Appl |
| 21 | 1121 | 100.0 | 582 | 15 US-10-232-231-92  | Sequence 92, Appl |
| 22 | 1121 | 100.0 | 582 | 15 US-10-232-233-92  | Sequence 92, Appl |
| 23 | 1121 | 100.0 | 582 | 15 US-10-216-165-92  | Sequence 92, Appl |
| 24 | 1121 | 100.0 | 582 | 15 US-10-218-956-92  | Sequence 92, Appl |
| 25 | 1121 | 100.0 | 582 | 15 US-10-219-468-92  | Sequence 92, Appl |
| 26 | 1121 | 100.0 | 582 | 15 US-10-219-478-92  | Sequence 92, Appl |
| 27 | 1121 | 100.0 | 582 | 15 US-10-219-536-92  | Sequence 92, Appl |
| 28 | 1121 | 100.0 | 582 | 15 US-10-233-205-92  | Sequence 92, Appl |
| 29 | 1121 | 100.0 | 582 | 15 US-10-219-072-92  | Sequence 92, Appl |
| 30 | 1121 | 100.0 | 582 | 15 US-10-219-470-92  | Sequence 92, Appl |
| 31 | 1121 | 100.0 | 582 | 15 US-10-219-474-92  | Sequence 92, Appl |
| 32 | 1121 | 100.0 | 582 | 15 US-10-219-524-92  | Sequence 92, Appl |
| 33 | 1121 | 100.0 | 582 | 15 US-10-219-528-92  | Sequence 92, Appl |
| 34 | 1121 | 100.0 | 582 | 15 US-10-227-880-92  | Sequence 92, Appl |
| 35 | 1121 | 100.0 | 582 | 15 US-10-227-881-92  | Sequence 92, Appl |
| 36 | 1121 | 100.0 | 582 | 15 US-10-227-882-92  | Sequence 92, Appl |
| 37 | 1121 | 100.0 | 582 | 15 US-10-230-436-92  | Sequence 92, Appl |
| 38 | 1121 | 100.0 | 582 | 15 US-10-232-223-92  | Sequence 92, Appl |
| 39 | 1121 | 100.0 | 582 | 15 US-10-232-225-92  | Sequence 92, Appl |
| 40 | 1121 | 100.0 | 582 | 15 US-10-232-227-92  | Sequence 92, Appl |
| 41 | 1121 | 100.0 | 582 | 15 US-10-232-229-92  | Sequence 92, Appl |
| 42 | 1121 | 100.0 | 582 | 15 US-10-232-234-92  | Sequence 92, Appl |
| 43 | 1121 | 100.0 | 582 | 15 US-10-219-060-92  | Sequence 92, Appl |
| 44 | 1121 | 100.0 | 582 | 15 US-10-223-085-372 | Sequence 92, Appl |
| 45 | 1121 | 100.0 | 582 | 15 US-10-216-160-92  | Sequence 92, Appl |

## ALIGNMENTS

```

RESULT 1
US-09-892-949-18
; Sequence 18, Application US/09892949
; Publication No. US20030096339A1
GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prenehl, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-18
Query Match      100.0%; Score 1121; DB 11; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ALPAPENISCVYRKXLTCTWSPKSTSYQYVTKTVAEGEKDNTNNTSSSENA 60
      20 ALPAPENISCVYRKXLTCTWSPKSTSYQYVTKTVAEGEKDNTNNTSSSENA 79
QY      61 SCSFPLPRITPDNTTIEVEAENGDVVKSHTWTWRLNIAKTEBPDKIFRVKPVVGIKRM 120

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Db 80 SCSEFFLRITIPDNYTTEVAENGDGVTKSHMTYWRLENTAKTEPPKIFVKKVGLGKRM 139  
Qy 121 IOIEWIKPELAPVSSDKYTLRFRVTNSTSMWEVNFAPKRRKDKNQTYNLGLOPFTYVI 180  
Db 140 IOIEWIKPELAPVSSDKYTLRFRVTNSTSMWEVNFAPKRRKDKNQTYNLGLOPFTYVI 199  
Qy 181 ALRCVAKESKFWSDMSQEKMGTEEEAP 208  
Db 200 ALRCVAKESKFWSDMSQEKMGTEEEAP 227

## RESULT 2

US-10-216-163-92  
Sequence 92, Application US/10216163  
Publication No. US20030149239A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC79  
CURRENT APPLICATION NUMBER: US/10/216,163  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 92  
LENGTH: 582  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-216-163-92

Query Match 100.0%; Score 1121; DB 12; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4,6e-104;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPAKPNISCVYRRKRLCTWSPGKETSYQYTVKRTYAFGEKDNCTNSTSENRA 60  
Db 52 ALPAKPNISCVYRRKRLCTWSPGKETSYQYTVKRTYAFGEKDNCTNSTSENRA 111  
Qy 61 SCSEFFLRITIPDNYTTEVAENGDGVTKSHMTYWRLENTAKTEPPKIFVKKVGLGKRM 120  
Db 112 SCSEFFLRITIPDNYTTEVAENGDGVTKSHMTYWRLENTAKTEPPKIFVKKVGLGKRM 171

Qy 121 IOIEWIKPELAPVSSDKYTLRFRVTNSTSMWEVNFAPKRRKDKNQTYNLGLOPFTYVI 180  
Db 172 IOIEWIKPELAPVSSDKYTLRFRVTNSTSMWEVNFAPKRRKDKNQTYNLGLOPFTYVI 231  
Qy 181 ALRCVAKESKFWSDMSQEKMGTEEEAP 208  
Db 232 ALRCVAKESKFWSDMSQEKMGTEEEAP 259

## RESULT 3

US-10-227-884-92  
Sequence 92, Application US/10227884  
Publication No. US20030027988A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC79  
CURRENT APPLICATION NUMBER: US/10/227,884  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
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PRIOR FILING DATE: 1998-05-13  
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PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
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 PRIOR APPLICATION NUMBER: 60/108849  
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 PRIOR FILING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: 60/113296  
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 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: 60/146963  
 PRIOR FILING DATE: 1999-08-03  
 PRIOR APPLICATION NUMBER: 60/149320  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/149638  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/151733  
 PRIOR FILING DATE: 1999-08-31  
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 PRIOR APPLICATION NUMBER: 60/169445  
 PRIOR FILING DATE: 1999-12-07  
 PRIOR APPLICATION NUMBER: 60/169495  
 PRIOR FILING DATE: 1999-12-07  
 PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 4,66-104;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVVKRTYAFGEKHNDCTNNTSSSENRA 60  
 DB 52 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVVKRTYAFGEKHNDCTNNTSSSENRA 111

|    |     |   |     |
|----|-----|---|-----|
| Qy | 61  | SCSEFFERITIPONTNYIEVAENGDDVISHMTYRLLENIAATEBPKEFRKVPVLGIXKM | 120 |
| Db | 112 | SCSEFFERITIPONTNYIEVAENGDDVISHMTYRLLENIAATEBPKEFRKVPVLGIXKM | 171 |
| Qy | 121 | IOIEMIKPELAPVSSDKTYLPRATNYSIMMEVAFANRRKDXTNYLGLQJFFTEYVI    | 180 |
| Db | 172 | IOIEMIKPELAPVSSDKTYLPRATNYSIMMEVAFANRRKDXTNYLGLQJFFTEYVI    | 231 |
| Qy | 181 | ALRCAYVESKFMDSQOEKMGITEEAP                                  | 208 |
| Db | 232 | ALRCAYVESKFMDSQOEKMGITEEAP                                  | 259 |

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1      RESULT 4
2      US-10-230-163-92
3      Sequence 92, Application US/10230163
4      Publication No. US2003003635A1
5      GENERAL INFORMATION:
6      APPLICANT: Baker, Kevin P.
7      APPLICANT: Deenoyers, Luc
8      APPLICANT: Gerritsen, Mary
9      APPLICANT: Goddard, Audrey
10     APPLICANT: Godowski, Paul J.
11     APPLICANT: Grimaldi, J. Christopher
12     APPLICANT: Gurney, Austin L.
13     APPLICANT: Smith, Victoria
14     APPLICANT: Stephan, Jean-Philippe F.
15     APPLICANT: Watanabe, Colin L.
16     APPLICANT: Wood, William I.
17     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
18     FILE REFERENCE: P3530P1C96
19     CURRENT APPLICATION NUMBER: US/10/230,163
20     CURRENT FILING DATE: 2002-08-28
21     PRIOR APPLICATION NUMBER: 10/119,480
22     PRIOR FILING DATE: 2002-04-09
23     PRIOR APPLICATION NUMBER: 60/059113
24     PRIOR FILING DATE: 1997-09-17
25     PRIOR APPLICATION NUMBER: 60/062287
26     PRIOR FILING DATE: 1997-10-17
27     PRIOR APPLICATION NUMBER: 60/063549
28     PRIOR FILING DATE: 1997-10-28
29     PRIOR APPLICATION NUMBER: 60/064103
30     PRIOR FILING DATE: 1997-10-31
31     PRIOR APPLICATION NUMBER: 60/069873
32     PRIOR FILING DATE: 1997-12-17
33     PRIOR APPLICATION NUMBER: 60/078910
34     PRIOR FILING DATE: 1998-03-20
35     PRIOR APPLICATION NUMBER: 60/079294
36     PRIOR FILING DATE: 1998-03-25
37     PRIOR APPLICATION NUMBER: 60/079656
38     PRIOR FILING DATE: 1998-03-26
39     PRIOR APPLICATION NUMBER: 60/079728
40     PRIOR FILING DATE: 1998-03-27
41     PRIOR APPLICATION NUMBER: 60/081819
42     PRIOR FILING DATE: 1998-04-15
43     PRIOR APPLICATION NUMBER: 60/081955
44     PRIOR FILING DATE: 1998-04-15
45     PRIOR APPLICATION NUMBER: 60/082804
46     PRIOR FILING DATE: 1998-04-22
47     PRIOR APPLICATION NUMBER: 60/084441
48     PRIOR FILING DATE: 1998-05-06
49     PRIOR APPLICATION NUMBER: 60/085323
50     PRIOR FILING DATE: 1998-05-13
51     PRIOR APPLICATION NUMBER: 60/085579
52     PRIOR FILING DATE: 1998-05-15
53     PRIOR APPLICATION NUMBER: 60/086392
54     PRIOR FILING DATE: 1998-05-22
55     PRIOR APPLICATION NUMBER: 60/089532
56     PRIOR FILING DATE: 1998-06-17
57     PRIOR APPLICATION NUMBER: 60/089538
58     PRIOR FILING DATE: 1998-06-17

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|                                       |                                       |                               |                                      |                               |                                       |                               |                                      |                               |                                       |                               |                                      |                               |                                       |                               |                                      |                               |                                      |                               |                                      |                               |                                      |                               |                                      |                               |                                       |                               |                                      |                               |                                      |                               |                                       |                               |                                      |                               |                                       |                               |                                       |                               |                                      |                               |                                      |                               |                                      |                               |                                      |                               |                                      |                               |                                       |                               |                                       |                               |                                      |                               |                                       |                               |                                      |                               |                                      |                               |                                       |                               |                                      |                               |                                      |                               |                                      |                               |                                       |                               |                                      |                               |                                       |
|---------------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|-------------------------------|--------------------------------------|-------------------------------|---------------------------------------|
| PRIOR APPLICATION NUMBER: 60/08989053 | PRIOR APPLICATION NUMBER: 60/09304727 | PRIOR FILING DATE: 1998-06-18 | PRIOR APPLICATION NUMBER: 60/0905577 | PRIOR FILING DATE: 1998-06-24 | PRIOR APPLICATION NUMBER: 60/09056131 | PRIOR FILING DATE: 1998-06-24 | PRIOR APPLICATION NUMBER: 60/0906591 | PRIOR FILING DATE: 1998-06-25 | PRIOR APPLICATION NUMBER: 60/09065955 | PRIOR FILING DATE: 1998-06-25 | PRIOR APPLICATION NUMBER: 60/0919622 | PRIOR FILING DATE: 1998-07-07 | PRIOR APPLICATION NUMBER: 60/09353020 | PRIOR FILING DATE: 1998-08-04 | PRIOR APPLICATION NUMBER: 60/0953318 | PRIOR FILING DATE: 1998-08-04 | PRIOR APPLICATION NUMBER: 60/0959166 | PRIOR FILING DATE: 1998-08-10 | PRIOR APPLICATION NUMBER: 60/0961466 | PRIOR FILING DATE: 1998-08-11 | PRIOR APPLICATION NUMBER: 60/0967931 | PRIOR FILING DATE: 1998-08-17 | PRIOR APPLICATION NUMBER: 60/0979866 | PRIOR FILING DATE: 1998-08-26 | PRIOR APPLICATION NUMBER: 60/09854444 | PRIOR FILING DATE: 1998-08-31 | PRIOR APPLICATION NUMBER: 60/0995666 | PRIOR FILING DATE: 1998-09-09 | PRIOR APPLICATION NUMBER: 60/0995986 | PRIOR FILING DATE: 1998-09-09 | PRIOR APPLICATION NUMBER: 60/09980303 | PRIOR FILING DATE: 1998-09-10 | PRIOR APPLICATION NUMBER: 60/0998111 | PRIOR FILING DATE: 1998-09-10 | PRIOR APPLICATION NUMBER: 60/09981212 | PRIOR FILING DATE: 1998-09-10 | PRIOR APPLICATION NUMBER: 60/09981616 | PRIOR FILING DATE: 1998-09-10 | PRIOR APPLICATION NUMBER: 60/1000388 | PRIOR FILING DATE: 1998-09-11 | PRIOR APPLICATION NUMBER: 60/1003855 | PRIOR FILING DATE: 1998-09-15 | PRIOR APPLICATION NUMBER: 60/1003900 | PRIOR FILING DATE: 1998-09-15 | PRIOR APPLICATION NUMBER: 60/1006227 | PRIOR FILING DATE: 1998-09-16 | PRIOR APPLICATION NUMBER: 60/1008488 | PRIOR FILING DATE: 1998-09-18 | PRIOR APPLICATION NUMBER: 60/10091919 | PRIOR FILING DATE: 1998-09-17 | PRIOR APPLICATION NUMBER: 60/10147777 | PRIOR FILING DATE: 1998-09-23 | PRIOR APPLICATION NUMBER: 60/1017388 | PRIOR FILING DATE: 1998-09-24 | PRIOR APPLICATION NUMBER: 60/10174111 | PRIOR FILING DATE: 1998-09-24 | PRIOR APPLICATION NUMBER: 60/1017866 | PRIOR FILING DATE: 1998-09-25 | PRIOR APPLICATION NUMBER: 60/1019166 | PRIOR FILING DATE: 1998-09-24 | PRIOR APPLICATION NUMBER: 60/10192222 | PRIOR FILING DATE: 1998-09-24 | PRIOR APPLICATION NUMBER: 60/1061788 | PRIOR FILING DATE: 1998-10-28 | PRIOR APPLICATION NUMBER: 60/1062488 | PRIOR FILING DATE: 1998-10-29 | PRIOR APPLICATION NUMBER: 60/1064644 | PRIOR FILING DATE: 1998-10-30 | PRIOR APPLICATION NUMBER: 60/10690505 | PRIOR FILING DATE: 1998-11-03 | PRIOR APPLICATION NUMBER: 60/1087877 | PRIOR FILING DATE: 1998-11-17 | PRIOR APPLICATION NUMBER: 60/10880101 |
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PRIOR FILING DATE: 1998-11-17  
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PRIOR FILING DATE: 1999-07-28  
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PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/149320  
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PRIOR APPLICATION NUMBER: 60/149638  
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PRIOR APPLICATION NUMBER: 60/151733  
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PRIOR APPLICATION NUMBER: 60/164418  
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PRIOR APPLICATION NUMBER: 60/166361  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/169445  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4,6e-104;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALPAKENISCVYYRKMLCTWSPGKETSYYQYTVKRYAFGEKHDNCTNSENRA 60  
DB 52 ALPAKENISCVYYRKMLCTWSPGKETSYYQYTVKRYAFGEKHDNCTNSENRA 111  
QY 61 SCSFPLRITPIDNTTIEVEANGDVIKSHMTYRLNENIAKTEPPKIPRVKPVIGIKEM 120  
DB 112 SCSFPLRITPIDNTTIEVEANGDVIKSHMTYRLNENIAKTEPPKIPRVKPVIGIKEM 171  
QY 121 IOIEWTKPELAVSSDLKTLTFRYVNSTSWMEVAFKARKKRNQYNTLTGQPFTEYIT 180  
DB 172 IOIEWTKPELAVSSDLKTLTFRYVNSTSWMEVAFKARKKRNQYNTLTGQPFTEYIT 231  
QY 181 ALRCAYKESKFWSDMSOEGMGTEEEAP 208  
DB 232 ALRCAYKESKFWSDMSOEGMGTEEEAP 259

RESULT 5  
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; Sequence 92, Application US/10230338  
; Publication No. US20030044934A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PLC92  
; CURRENT APPLICATION NUMBER: US/10/230,338  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; Remaining Prior Application data removed - See File Wrapper or PAM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 92  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-230-338-92

Query Match 100.0%; Score 1121; DB 15; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4,6e-104;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALPAKENISCVYYRKMLCTWSPGKETSYYQYTVKRYAFGEKHDNCTNSENRA 60





;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P350P1C72  
;; CURRENT APPLICATION NUMBER: US/10/227, 873  
;; PRIOR FILING DATE: 2002-08-26, 873  
;; PRIOR APPLICATION NUMBER: 10/119,480  
;; PRIOR FILING DATE: 2002-04-09  
;; PRIOR APPLICATION NUMBER: 60/059113  
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;; PRIOR APPLICATION NUMBER: 60/062287  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063549  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/064103  
;; PRIOR FILING DATE: 1997-10-31  
;; PRIOR APPLICATION NUMBER: 60/069873  
;; PRIOR FILING DATE: 1997-12-17  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079294  
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;; PRIOR APPLICATION NUMBER: 60/079656  
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;; PRIOR APPLICATION NUMBER: 60/079728  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/081819  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081955  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/082804  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/084441  
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;; PRIOR APPLICATION NUMBER: 60/085323  
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;; PRIOR APPLICATION NUMBER: 60/086392  
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;; PRIOR APPLICATION NUMBER: 60/090691  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/095302  
;; PRIOR FILING DATE: 1998-08-04  
;; PRIOR APPLICATION NUMBER: 60/095316  
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;; PRIOR APPLICATION NUMBER: 60/096146  
;; PRIOR FILING DATE: 1998-08-11  
;; PRIOR APPLICATION NUMBER: 60/096791  
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PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4,6e-104;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTLCTWSPKETSSTQYTVKRTAFGEKNDCTNSTSENRA 60  
DB 52 ALPAKPNISCVYYRRKNTLCTWSPKETSSTQYTVKRTAFGEKNDCTNSTSENRA 111  
QY 61 SCSEFLPRITIPNVTIEVEAENGDDGVKSHMTYMRLENIATKEPPKIFVKGVLGIKRM 120  
DB 112 SCSEFLPRITIPNVTIEVEAENGDDGVKSHMTYMRLENIATKEPPKIFVKGVLGIKRM 171  
QY 121 IQIEWIKPELAPVSDIKYTLRFRYVNSTSMWEVNFAPKRNKDNQYTNLTGLQPTFEYVI 180  
DB 172 IQIEWIKPELAPVSDIKYTLRFRYVNSTSMWEVNFAPKRNKDNQYTNLTGLQPTFEYVI 231  
QY 181 ALCAVAKESKFWSDMSQERKMGTEEARP 208  
DB 232 ALCAVAKESKFWSDMSQERKMGTEEARP 259

## RESULT 11

US-10-227-883-92  
Sequence 92, Application US/10227883  
Publication No. US20030073817A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Geritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gueney, Auelin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC78  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: US/10/227,883  
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; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4.6e-104; Indels 0; Gaps 0;  
Matches 208; Conservative 0; Mismatches 0;

QY 1 ALPAKPNISCVYYRKNLTCTWSPKETSYYQYVKTAFGEKHDNCTTNSSTSENRA 60  
DB 52 ALPAKPNISCVYYRKNLTCTWSPKETSYYQYVKTAFGEKHDNCTTNSSTSENRA 111  
QY 61 SCGFLLPRITIPDNYTIEVEAENGQGVIKSHMTYMLENIATPEPKIFRVPVIGIKM 120  
DB 112 SCGFLLPRITIPDNYTIEVEAENGQGVIKSHMTYMLENIATPEPKIFRVPVIGIKM 171  
QY 121 IOEWIKPELAPSSSLKTLRRTYNTSNMSEVNFAPKRNKQYNTLTGQPFTEYVI 180  
DB 172 IOEWIKPELAPSSSLKTLRRTYNTSNMSEVNFAPKRNKQYNTLTGQPFTEYVI 231  
QY 181 ALRCAYKESKFSWSDSQEKGMTTEEP 208  
DB 232 ALRCAYKESKFSWSDSQEKGMTTEEP 259

RESULT 12  
US-10-219-076-92  
; Sequence 92, Application US/10219076  
; Publication No. US20030078379A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C62
; CURRENT APPLICATION NUMBER: US/10/219,076
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
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; PRIOR APPLICATION NUMBER: 60/064103
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
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; ORGANISM: Homo Sapien
US-10-219-076-92

Query Match          100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVRYAFAEKKDNCCTNSISENRA 60
DB 52 ALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVRYAFAEKKDNCCTNSISENRA 111
QY 61 SCSEFLPRTITPNNTTEVAENGDDGVKSHMTYWRLENTAKTEPPKIFVKKVLGIKRM 120
DB 112 SCSEFLPRTITPNNTTEVAENGDDGVKSHMTYWRLENTAKTEPPKIFVKKVLGIKRM 171
QY 121 IQEWIKPELAPVSDKTYLRFRTVNSTSMWEVNPFAKKNQKQNTNLGLQPTFEYVY 180
DB 172 IQEWIKPELAPVSDKTYLRFRTVNSTSMWEVNPFAKKNQKQNTNLGLQPTFEYVY 231
QY 181 ALRCAVSKSKFWSQKMGTEEAR 208
DB 232 ALRCAVSKSKFWSQKMGTEEAR 259

RESULT 13
US-10-230-434-92
; Sequence 92, Application US/10230434
; Publication No. US20030078380A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
```

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C62
; CURRENT APPLICATION NUMBER: US/10/230,434
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; PRIOR APPLICATION NUMBER: 60/113605
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; PRIOR FILING DATE: 1998-12-23
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; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
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; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR APPLICATION NUMBER: 60/125259
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; PRIOR APPLICATION NUMBER: 60/125775
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; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
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; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4,6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ALPAKRENTSCVYYKONLCTWSPKETSQYTYKRYARGKHNDCTTSSSENBA 60
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Db      52  ALPAKRENTSCVYYKONLCTWSPKETSQYTYKRYARGKHNDCTTSSSENBA 111
      |||||||
QY      61  SCSEFLPRITIPDNTYTEAEANGDVIKSHNTYWRLENIATTEPKIFRVAPVLGIKSM 120
      |||||||
Db      112 SCSEFLPRITIPDNTYTEAEANGDVIKSHNTYWRLENIATTEPKIFRVAPVLGIKSM 171
      |||||||
QY      121 IQIEWIKPELAPVSSDLKTLRPRYVNSTSMWEVNFAPKRRKDKQNTYNTGLQPTFEYVI 180
      |||||||
Db      172 IQIEWIKPELAPVSSDLKTLRFRFTVNSTSMWEVNFAPKRRKDKQNTYNTGLQPTFEYVI 231
      |||||||
QY      181 ALRCAYKESKFWSDWSQERMGTEEBAP 208
      |||||||
Db      232 ALRCAYKESKFWSDWSQERMGTEEBAP 259
      |||||||

RESULT 14
US-10-219-003-92
; Sequence 92, Application US/10219003
; Publication No. US20030088063A1
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GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Geriltsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, U. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Matanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530P1C12  
CURRENT FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: US/10/219,003  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-10-28  
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PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
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PRIOR FILING DATE: 1998-12-23  
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PRIOR APPLICATION NUMBER: 60/115565  
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PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549

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; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
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; PRIOR APPLICATION NUMBER: 60/131270
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; PRIOR APPLICATION NUMBER: 60/131445
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; PRIOR APPLICATION NUMBER: 60/169445
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPENISCVYYRRKNTCTWSPGKETSQYTVKRTYAFGEKHNDCTNNTSSSENRA 60
DB 52 ALPAKPENISCVYYRRKNTCTWSPGKETSQYTVKRTYAFGEKHNDCTNNTSSSENRA 111
QY 61 SCSEFLPRITIPDNTTIEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 120
DB 112 SCSEFLPRITIPDNTTIEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 171
QY 121 IOIEWIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRRKDKNQTNLGLQPFTEYVI 180
DB 172 IOIEWIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRRKDKNQTNLGLQPFTEYVI 231
QY 181 ALRCAYESKRFWSQKMGTEBEAP 208
DB 232 ALRCAYESKRFWSQKMGTEBEAP 259
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RESULT 15
US-10-219-075-92
; Sequence 92. Application US/10219075
; Publication No. US2003008064A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurley, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C61
; CURRENT APPLICATION NUMBER: US/10/219,075
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-075-92

Query Match      100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPENISCVYYRRKNTCTWSPGKETSQYTVKRTYAFGEKHNDCTNNTSSSENRA 60
DB 52 ALPAKPENISCVYYRRKNTCTWSPGKETSQYTVKRTYAFGEKHNDCTNNTSSSENRA 111
QY 61 SCSEFLPRITIPDNTTIEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 120
DB 112 SCSEFLPRITIPDNTTIEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 171
QY 121 IOIEWIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRRKDKNQTNLGLQPFTEYVI 180
DB 172 IOIEWIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRRKDKNQTNLGLQPFTEYVI 231
QY 181 ALRCAYESKRFWSQKMGTEBEAP 208
DB 232 ALRCAYESKRFWSQKMGTEBEAP 259
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Search completed: August 18, 2003, 13:33:22  
Job time : 28.5067 secs



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C:Accession: J36337  
R:Hihi, M.; Murakami, M., Saito, M., Hirano, T., Taga, T., Kishimoto, T.  
Cell 63, 1149-1157, 1990  
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130  
A:Reference number: A36337; MUID:91084844; PMID:2261537  
A:Accession: A36337  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-918 <HTB>  
A:Cross-references: GB:M57230, NID:G186353, PIDN:AA59155.1, PID:G186354  
C:Genetics:  
A:Gene: GDB:IL6ST, GP130  
A:Cross-references: GDB:126725, OMIM:600694  
A:Map position: Sg11-Sg11  
C:Superfamily: cytokine receptor homology  
C:Keywords: glycoprotein; membrane protein  
C:Keywords: cytokine receptor homology <CRS>  
I:31-316/Domain: cytokine receptor homology

|                       |                  |                    |            |             |
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| Query March           | 24.0%;           | Score 268.5;       | DB 2;      | Length 918; |
| Best Local Similarity | 30.3%;           | Pred. No. 4.1e-15; |            |             |
| Matches 66;           | Conservative 47; | Mismatches 76;     | Indels 29; | Gaps 11     |

QY 3 P A P E N I S C V Y Y X R K N L A C T W S P G S E T S Y - T Q Y A W K - - - R T Y A G E - - - K H D - - - N C T T N 52  
 126 P E P K N L S C I V N E G K M C R C E D G G E T H L E T N F T L K S E W A T H K F A D C K A R D T P P S C T D 185

Dy 53 SSSSENKASCSFLLPRITTDNYTTEVEAEAGDGVKS-HMTYWRLENIATKEPPKIFRV 111  
||| : | |||| : | : : |  
Db 186 YST-----VYFY-----NIEWVEAENALGKTSDHINFDPYKYV-KENPPHNLISV 230

Df QY  
112 KPLVGIKRMQIENIKPELAPVSSDLKYTLRFRVTNVSSTWHEVNFANRKDKNQTYNLTG 171  
: ::: | : | ||| ::|| ::|| : :  
Dg 231 INSEELSLIKLTWTNPSPISKVII-TKYNIQRYTKDASTWGIP-PEDTASRSSFTVQD 288

Qy 172 LQPFTEYVIALRCAYKESK-FMSDMSQEKMTTEEAR 208  
|:|||||:|::|:|||||:|:|:  
Db 289 LKPFTEYVIRICMKEDGKGWSDWSEASGITYEDRP 326

### RESULT 3

interleukin-6 signal transducing molecule gp130 - rat  
 C.Species: Rattus norvegicus (Norway rat)  
 C.Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Jul-2000  
 C.Accession: A44257  
 R.Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.  
 Genomics 14, 666-672, 1992  
 A.Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing  
 A.Reference number: A44257; MUID:93052397; PMID:1427893  
 A.Accession: A44257  
 A.Status: preliminary; not compared with conceptual translation  
 A.Molecule type: mRNA  
 A.Residues: 1-918 <MAN>  
 A:Note: Experimental source: liver  
 A:Note: sequence extracted from NCBI backbone (NCBIF:118488)  
 C:Superfamily: cytokine receptor homology  
 C.Keywords: transmembrane protein  
 C:134-315/Domain: cytokine receptor homology <CR>

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 22.3%            | Score 250;         | DB 2;      | Length 918; |
| Best Local Similarity | 31.4%            | Pred. No. 1.6e-13; |            |             |
| Matches 66;           | Conservative 42; | Mismatches 88;     | Indels 14; | Gaps 9;     |

Dy            3 PAAPENISCVYYRKNLTCTWSPGKETS Y -TQYTVKRTYAAGEKHDCNTTNSSSTSENBAS 61  
| | | : | | | : | | : | | |  
Db         126 PDPIPTNLSCIVNEGKNMLQQUDPGETYLENNYTLKS EWA -TEKFDPDCKTKHGS -----S 180

QY 62 CSF-FLPRTTIPDNYTIEVAENGSGVICKSMTYMLENIAKTEPPKIFRYKPVLTGIKRM 120

Db 181 CMNGYTPIVFV-NIEWVTEALNALGNVSSSEPIINFPVDKVKPSPHNLSTVNSEELSSI 238

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QY      121 IQEWIKBELAPVSSDLKTYLRFRTVNSTSMMEVNFAPKNRKDKNQTYNLGTGQPFTEVI 180
      :: | : | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |

```

D6  
229 LKLANVNSGLSDILA-LKSDIOYRKDKASTWIQVPL-EDTVSBRISFTYQDLKPFEIYYF 256

O7  
181 ALRCAVKES--KFMSDMSOEKKMGMTTEEPAP 208  
:::|||||: ||||:  
297 RIR-SIKENGKGYSMDMSEASGTTYEDRP 325

## RESULT 4

prolactin receptor precursor - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Jul-2000  
C.Accession: I77525  
R.Davis, J.A.; Linzer, D.I.H.  
Mol. Endocrinol. 3, 674-680, 1989  
A.Title: Expression of multiple forms of the prolactin receptor in mouse liver  
A.Reference number: I57659; MUID:89261824; PMID:2725531  
A.Accession: I77525  
A.Status: Preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-292 <RES>  
A.Cross-references: GB:M2959; NID:G200481; PIDN:AAA39977.1; PID:G200482  
C.Superfamily: cytokine receptor homology  
F31-216/Domain: cytokine receptor homology <CRS>

|                       |        |                    |       |             |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match           | 17.0%; | Score 191;         | DB 2; | length 232; |
| Best Local Similarity | 27.8%; | Pred. No. 4.7e-09; |       |             |
| Matches               | 57;    | Conservative       | 92;   | Indels 18;  |
|                       |        | Mismatches         | 92;   | Gaps 10;    |

Db

|    |         |             |       |       |       |         |     |      |       |    |      |     |    |      |      |     |    |
|----|---------|-------------|-------|-------|-------|---------|-----|------|-------|----|------|-----|----|------|------|-----|----|
| 3  | PAKENIS | SCVYYRRKLLT | TWSPG | KETSY | -     | TOYIVRT | IVA | -    | FGEKD | -  | NCTN | SS  | TS | ENR  | 59   |     |    |
|    |         | :::         | :::   | :::   |       | :::     | ::: |      | :::   |    | :::  | ::: |    |      |      |     |    |
| 23 | PKKEIHK | RKSPDK      | ETFCW | NP    | PGSDG | L       | PL  | NYSL | -     | TS | AGE  | K   | NT | YECD | YKTS | SPN | 79 |

Db 60 -SCFSSKQYTSIMKTYIITVATNEMGSSSDPLVDVTYIVVEPEPRNRLTLEVKQLKDK 138

Oy 118 KRMQIEWIKPELAPVSS---DLKTLRPTVNSTSWMEVAFKKSKDKNTYNLGLQP 174  
::: :::::  
Db 139 KTYLVAKWLPPTLYDVKTGFTMEEIRLSSEADQM-EIHFTGHQTQ----EKVPDLYP 193

Qy 175 FTEYIALRCVAKESKRFMSDMSQEK 199  
::: : : : :  
Db 194 GKRLVQTRCK-PDHYGWSRMGQEK 217

## RESULT 5

prolactin receptor precursor - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Jul-2000  
C.Accession: I77524  
R.Davis, J.A.; Linzer, D.I.H.  
Mol. Endocrinol. 3, 674-680, 1989  
A.Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
A.Reference number: I57699; MUID:89261824; PMID:2725531  
A.Accession: I77524  
A.Status: Preliminary; translated from GB/EMBL/DBD  
A.Molecule type: mRNA  
A.Residues: 1-303 <RES>  
C.Cross-references: GB:M2958; NID:g200479; PIDN:AAA39976.1; PID:g200480  
C.Superfamily: cytokine receptor homology  
F31-216/Domain: cytokine receptor homology <CR>

|                       |        |                    |       |                     |
|-----------------------|--------|--------------------|-------|---------------------|
| Query Match           | 17.0%; | Score 191;         | DB 2; | Length 303;         |
| Best Local Similarity | 27.8%; | Pred. No. 4.9e-09; |       |                     |
| Matches               | 57;    | Conservative       | 92;   | Indels 18; Gaps 10; |
|                       |        | Mismatches         | 92;   |                     |

Db

```

3  PAKENISICVYYRNKLTCTWSPGKETS-Y-TOYTRRTVA-FGEKRD-NCTNNSSTSEN 59
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
23 PKEKEIHKRSPDKETFTCMNPNPGSDGGLPTNYSL--TYSKEGEKNTVECDYKTSQPN- 79
```

60 ASCSFFLPRTIPDNYTIEVEAENGDVIKSHMTYRWLRLENIATKTEBP--IPRVKPVLGI 117





A:Accession: A36116  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-610 <SH1>  
A:Cross-references: GB:M57668; NID:g20636; PIND:AAA41938.1; PID:g206367; GB:M607288  
C:Superfamily: cytokine receptor homology  
F31216/Domain: cytokine receptor homology <CRS>

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 16.1%;           | Score 181;         | DB 2;      | Length 610; |
| Best Local Similarity | 27.9%;           | Pred. No. 8.6e-08; |            |             |
| Matches 57;           | Conservative 35; | Mismatches 94;     | Indels 18; | Gaps 10;    |

```
OY      3 PAKPENISCVYYXKRNKFTGMSPGKEITS--TQTVKRYTA-FEKKD-NCTNSTRSENR 59
Db      23 PKPRLHKCRSPDKETFTCWANPNFGIDGLPTNYSL--TYSKGSKTTYECBPDYKTSGN- 79
OY      60 ASCSFFLRITIPDNVTIEVEAENGDSGVIKSHNTVRLNENIAKTEBPK--IFRKYVLGI 117
Db      80 -SCFSPSQYTSIMKIYIILFNATINQMCGSSSDPLVDVVIYEPEPRNLTLLEVKQLOK 138
OY      118 KRMIDIEWIKPELAPVSS---DLKTYLRRTYNSTNSWMEVNFPAKNKDKNQTYNLTLGLOP 174
Db      139 KYLYLVWKWSPPITIVTKGTGMFTMBEYELRIKLPEAEEM-EIHFIHGOTO----FKVDPYE 193
OY      175 FLEYVALRCNAVKSSEKFWMSDMSOE 198
Db      194 GOKYLVOGRCK-PDHGYMSRMSOE 216
```

RESULT 13  
JQ1655

prolactin receptor precursor - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
C/Accession: J01655  
R: Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K  
Biochem. Biophys. Res. Commun. 188, 480-486, 1992  
A/Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence  
A/Reference number: J01655; MUID:93075121; PMID:11445292  
A/Accession: J01655

A: Molecule type: mRNA  
A: Residues: 1-831 <TAN>  
A: Cross-references: DDBJ: D13154; NID: G222848; PIDD: BAA02439.1; PID: G222849  
A: Experimental source: Kidney  
C: Superfamily: cytokine receptor homology  
C: Keywords: glycoprotein; transmembrane protein  
F: 1-23/Domain: signal sequence #status predicted <SIG>  
F: 24-831/Product: prolactin receptor #status predicted <MAT>  
F: 36-219/Domain: cytokine receptor homology <CR81>  
F: 238-425/Domain: cytokine receptor homology <CR82>  
F: 438-462/Domain: transmembrane #status predicted <TM>  
F: 559, 91, 100, 112, 132, 262, 303, 315, 335, 647, 701, 800/Binding site: carbohydrate (Asn) (covalet

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 16.0%;           | Score 179.5;       | DB 2;      | Length 831; |
| Best Local Similarity | 26.7%;           | Pred. No. 1.7e-07; |            |             |
| Matches 54;           | Conservative 26; | Mismatches 109;    | Indels 13; | Gaps 5      |

QY 3 PAKPENISGVYVYRKULJCTWSPGKSTYS-TQTVVRIYA FGGKHONCTNSSTSENKAS 61

Db 231 PEKPTIKCRSPKEKETFTCMWRGDLGGHPYNTYLLYSKRGEGVYECPDYRAGPN--S 288

QY 62 CSFPLRATIPDNNTYEVAENGDDGVYIKSHMYTWRLBENLAKTEPP--KI PRVRYVLGIR 119

Db 289 CYFDKGGHSEFWITVITVATATWMSGNSSDPRHYDVTYIVQDPFNAVLTIELKPPINRKP 348

QY 120 MIQIEWIKPELAPVSS---DKYTLRFRVJNSTSMWEVNFAPKRRKQNTYNTLGLQFPT 176

Db 349 YLVLTWSPPLADVSGWLTILEYELTKKEGEGEWITIFVGGQGTQ-----YKNFSLNPGK 403

QY 177 EYVIALRCVAVKESKFWSDWSQE 198  
::|:| | | |  
Db 404 KYIQIHCKRPDHHGWSWSE 425

RESULT 14  
A30304

prolactin receptor 2 precursor - rabbit  
Mlternate names: prolactin receptor, mammary gland  
C/species: *Oryctolagus cuniculus* (domestic rabbit)  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Jul-2000

R.Ébèry, M.; Collicœur, C.; Lefi-Weynneis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin  
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989  
Article: Identification and sequence analysis of a second form of prolactin receptor by  
A:Reference number: A30304; PMID:69184578; PMID:2928321

A:Accession: A0304  
A:Molecule type: mRNA  
A:Residues: 1-616 <EED>  
A:Cross-references: GB:004510; NID:ig15669; PID:AAA3457.1; PID:ig15670  
R:Maters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
Int. J. Biochem. 22, 1089-1095, 1990  
A>Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor  
A:Reference number: A60380; MUID:91146782; PMID:2289615  
A:Accession: A0305

A: Molecule type: protein  
A: Residues: 41-58, 'X', 60-66, 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-154, 'XX', 160-161, 163-164, 166-167, 169-170, 172-173, 175-176, 178-179, 181-182, 184-185, 187-188, 190-191, 193-194, 196-197, 199-200, 202-203, 205-206, 208-209, 211-212, 214-215, 217-218, 220-221, 223-224, 226-227, 229-230, 232-233, 235-236, 238-239, 241-242, 244-245, 247-248, 250-251, 253-254, 256-257, 259-260, 262-263, 265-266, 268-269, 271-272, 274-275, 277-278, 280-281, 283-284, 286-287, 289-290, 292-293, 295-296, 298-299, 301-302, 304-305, 307-308, 310-311, 313-314, 316-317, 319-320, 322-323, 325-326, 328-329, 331-332, 334-335, 337-338, 340-341, 343-344, 346-347, 349-350, 352-353, 355-356, 358-359, 361-362, 364-365, 367-368, 370-371, 373-374, 376-377, 379-380, 382-383, 385-386, 388-389, 391-392, 394-395, 397-398, 400-401, 403-404, 406-407, 409-410, 412-413, 415-416, 418-419, 421-422, 424-425, 427-428, 430-431, 433-434, 436-437, 439-440, 442-443, 445-446, 448-449, 451-452, 454-455, 457-458, 460-461, 463-464, 466-467, 469-470, 472-473, 475-476, 478-479, 481-482, 484-485, 487-488, 490-491, 493-494, 496-497, 499-500, 502-503, 505-506, 508-509, 511-512, 514-515, 517-518, 520-521, 523-524, 526-527, 529-530, 532-533, 535-536, 538-539, 541-542, 544-545, 547-548, 550-551, 553-554, 556-557, 559-560, 562-563, 565-566, 568-569, 571-572, 574-575, 577-578, 580-581, 583-584, 586-587, 589-590, 592-593, 595-596, 598-599, 601-602, 604-605, 607-608, 610-611, 613-614, 616-617, 619-620, 622-623, 625-626, 628-629, 631-632, 634-635, 637-638, 640-641, 643-644, 646-647, 649-650, 652-653, 655-656, 658-659, 661-662, 664-665, 667-668, 670-671, 673-674, 676-677, 679-680, 682-683, 685-686, 688-689, 691-692, 694-695, 697-698, 700-701, 703-704, 706-707, 709-710, 712-713, 715-716, 718-719, 721-722, 724-725, 727-728, 730-731, 733-734, 736-737, 739-740, 742-743, 745-746, 748-749, 751-752, 754-755, 757-758, 760-761, 763-764, 766-767, 769-770, 772-773, 775-776, 778-779, 781-782, 784-785, 787-788, 790-791, 793-794, 796-797, 799-800, 802-803, 805-806, 808-809, 811-812, 814-815, 817-818, 820-821, 823-824, 826-827, 829-830, 832-833, 835-836, 838-839, 841-842, 844-845, 847-848, 850-851, 853-854, 856-857, 859-860, 862-863, 865-866, 868-869, 871-872, 874-875, 877-878, 880-881, 883-884, 886-887, 889-890, 892-893, 895-896, 898-899, 901-902, 904-905, 907-908, 910-911, 913-914, 916-917, 919-920, 922-923, 925-926, 928-929, 931-932, 934-935, 937-938, 940-941, 943-944, 946-947, 949-950, 952-953, 955-956, 958-959, 961-962, 964-965, 967-968, 970-971, 973-974, 976-977, 979-980, 982-983, 985-986, 988-989, 991-992, 994-995, 997-998, 1000-1001, 1003-1004, 1006-1007, 1009-1010, 1012-1013, 1015-1016, 1018-1019, 1021-1022, 1024-1025, 1027-1028, 1030-1031, 1033-1034, 1036-1037, 1039-1040, 1042-1043, 1045-1046, 1048-1049, 1051-1052, 1054-1055, 1057-1058, 1060-1061, 1063-1064, 1066-1067, 1069-1070, 1072-1073, 1075-1076, 1078-1079, 1081-1082, 1084-1085, 1087-1088, 1090-1091, 1093-1094, 1096-1097, 1099-1100, 1102-1103, 1105-1106, 1108-1109, 1111-1112, 1114-1115, 1117-1118, 1120-1121, 1123-1124, 1126-1127, 1129-1130, 1132-1133, 1135-1136, 1138-1139, 1141-1142, 1144-1145, 1147-1148, 1150-1151, 1153-1154, 1156-1157, 1159-1160, 1162-1163, 1165-1166, 1168-1169, 1171-1172, 1174-1175, 1177-1178, 1180-1181, 1183-1184, 1186-1187, 1189-1190, 1192-1193, 1195-1196, 1198-1199, 1201-1202, 1204-1205, 1207-1208, 1210-1211, 1213-1214, 1216-1217, 1219-1220, 1222-1223, 1225-1226, 1228-1229, 1231-1232, 1234-1235, 1237-1238, 1240-1241, 1243-1244, 1246-1247, 1249-1250, 1252-1253, 1255-1256, 1258-1259, 1261-1262, 1264-1265, 1267-1268, 1270-1271, 1273-1274, 1276-1277, 1279-1280, 1282-1283, 1285-1286, 1288-1289, 1291-1292, 1294-1295, 1297-1298, 1299-1300, 1302-1303, 1305-1306, 1308-1309, 1311-1312, 1314-1315, 1317-1318, 1320-1321, 1323-1324, 1326-1327, 1329-1330, 1332-1333, 1335-1336, 1338-1339, 1341-1342, 1344-1345, 1347-1348, 1350-1351, 1353-1354, 1356-1357, 1359-1360, 1362-1363, 1365-1366, 1368-1369, 1371-1372, 1374-1375, 1377-1378, 1380-1381, 1383-1384, 1386-1387, 1389-1390, 1392-1393, 1395-1396, 1398-1399, 1401-1402, 1

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 15.1%;           | Score 169;         | DB 2;      | Length 616; |
| Best Local Similarity | 29.3%;           | Pred. No. 9.4e-07; |            |             |
| Matches 60;           | Conservative 27; | Mismatches 98;     | Indels 20; | Gaps 11     |

QY 3 PAKPENISCVYRRNRKLNCTCS PGKSTSY -POYAKRTY -ARGE -KHNCNTNSSTSEN 58  
 Db 28 PGKPPIFPCRSBEKKTFTCCWRPRADGGLPNTYTL--TYHKEGETITHE-CDYKTYGSEN 84  
 QY 59 RASGCFPLPRITIPDNYTIEVEANGDGVIKSHMTYMLENIATAEPP-KIFRYKPVLG 116  
 Db 85--SCYFSKSKHSIMWTIYIITVNATQWSSVADPRYVDVYIVEDPDPVNLITLEVGHPEP 142  
 QY 117 IKRMQIMWIKPELAPVSS---DLKTYTRFRPVNSTSMVEUNFAKORKDKQNTLTGQ 173  
 Db 143 RKPYLMTVMLEPPTLVDVRSGLMLTQYELRLKPEKAAEW-ETHEFA-----GQOTOFKILSLEY 197  
 QY 174 PTEEVIALRCVAKESKFMDSKCE 198  
 Db 198 PGQKTLVQVRCK-PDHGFWSVWSPE 221

RESULT 15  
B38252

granulocyte colony-stimulating factor receptor precursor (clone pHQ2) - human  
C.Species: *Homo sapiens* (man)  
C.Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 05-Nov-1999  
C.Accession: B38252  
R.Fukunaga, R. I. Seto, Y. I. Mizushima, S. I. Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990  
Article: Three different mRNAs encoding human granulocyte colony-stimulating factor receptor  
A.Reference numbers: A38252, MUID:91062348, PMID:11701053

```
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-771 <FUK>
```

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 14.8%;           | Score 166;         | DB 2;      | Length 771; |
| Best Local Similarity | 27.1%;           | Pred. No. 2.3e-06; |            |             |
| Matches 64;           | Conservative 22; | Mismatches 96;     | Indels 54; | Gaps 10     |

```

QY      3 PAKPENISCVYYRKNLT-----CTWSPGKETSJ-TQYIVKRTYAFGEKHNDCTNSST- 55
Db      123 PAIPHNLSCL-----MNLTSLSLQOMEPGPETHLPFSFTLKSPKSRG---NCOTQGDST 174
QY      56 -----SENBRASCSEFLPRITIPNDYITEVAENGDVIKSHMTYWRLENIAKTEPPKIFR 110
Db      175 LDCVPKDGQSHCCIPRKHLLIYQNMGIWQAEANALGTSMSPOLCLDPMDVVKLEPPMLRT 234
QY      111 VKPVLGIKRMIIQIEWIKPELAPVSS-----DLKYTLRFRTV-NSTSWME 153
Db      235 MDP-----SPEAAPQOAGCLQLCMEBWPQGLHINQKCELRHKPQGEASWAL 281
QY      154 VNFAPKRNKDNQTYNLTGLQPFTEYIALRC-AVKESKFWSDSQOEKMGTEEEAP 208
Db      282 VG---PLPLEALQYELCGLLPATAYTLQIRCIWPLPGHWSDWSPSLRLRTERAP 334

```

Search completed: August 18, 2003, 13:31:21  
 Job time : 30.1496 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:27 ; Search time 15.81 seconds  
(without alignments)  
618.695 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_20\_227

Perfect score: 1121  
Sequence: 1 ALPAKPENISCVYYRRKNLT.....SKFMSDWSQEKMGKMTTEAP 208

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt 41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 271.5 | 24.2        | 917    | IL6B_MOUSE | Q00560 mus musculu |
| 2          | 268.5 | 24.0        | 918    | IL6B_HUMAN | P40189 homo sapien |
| 3          | 250   | 22.3        | 918    | IL6B_RAT   | P40190 rattus norv |
| 4          | 191   | 17.0        | 608    | PRLR_MOUSE | Q08501 mus musculu |
| 5          | 190.5 | 17.0        | 830    | PRLR_COLLI | Q90374 columba liv |
| 6          | 187   | 16.7        | 581    | PRLR_CEREL | Q28235 cervus elap |
| 7          | 185   | 16.5        | 581    | PRLR_SHEEP | Q46561 ovis aries  |
| 8          | 184   | 16.4        | 862    | IL25_HUMAN | Q99665 homo sapien |
| 9          | 183   | 16.3        | 581    | PRLR_BOVIN | Q28172 bos taurus  |
| 10         | 181   | 16.1        | 610    | PRLR_RAT   | P05710 rattus norv |
| 11         | 179.5 | 16.0        | 831    | PRLR_CHICK | Q04594 gallus gall |
| 12         | 176.5 | 15.7        | 831    | PRLR_MELGA | Q91094 melagris g  |
| 13         | 174.5 | 15.6        | 874    | IL25_MOUSE | P97378 mus musculu |
| 14         | 169   | 15.1        | 616    | PRLR_RABIT | P14787 oryctolagus |
| 15         | 166   | 14.8        | 836    | GCSR_HUMAN | Q99672 homo sapien |
| 16         | 156.5 | 14.0        | 424    | IL31_MOUSE | Q09030 mus musculu |
| 17         | 153   | 13.6        | 622    | PRLR_HUMAN | P16471 homo sapien |
| 18         | 152.5 | 13.6        | 1097   | LIFR_HUMAN | P42702 homo sapien |
| 19         | 151   | 13.5        | 837    | GCSR_MOUSE | P40223 mus musculu |
| 20         | 150.5 | 13.4        | 372    | CNTR_RAT   | Q08406 rattus norv |
| 21         | 150.5 | 13.4        | 1092   | LIFR_MOUSE | P42703 mus musculu |
| 22         | 150   | 13.4        | 630    | PRLR_ORENI | Q91513 oreochromis |
| 23         | 143.5 | 12.8        | 372    | CNTR_HUMAN | P26992 homo sapien |
| 24         | 137   | 12.2        | 427    | IL31_HUMAN | P78552 homo sapien |
| 25         | 127.5 | 11.4        | 362    | CNTR_CHICK | P51641 gallus gall |
| 26         | 121.5 | 10.8        | 468    | IL6A_HUMAN | P08887 homo sapien |
| 27         | 121   | 10.8        | 380    | IL33_HUMAN | Q14627 homo sapien |
| 28         | 121   | 10.8        | 380    | IL33_MOUSE | P26954 mus musculu |
| 29         | 117.5 | 10.5        | 638    | GHR_RABIT  | P19941 oryctolagus |
| 30         | 117.5 | 10.5        | 1162   | LIFR_RAT   | Q62959 rattus norv |
| 31         | 117   | 10.4        | 460    | IL6A_MOUSE | P22272 mus musculu |
| 32         | 116   | 10.3        | 896    | CYRB_MOUSE | P26955 mus musculu |
| 33         | 115   | 10.3        | 897    | CYRB_HUMAN | P32927 homo sapien |

|    |       |      |      |   |            |                    |
|----|-------|------|------|---|------------|--------------------|
| 34 | 114   | 10.2 | 608  | 1 | GHR_CHICK  | Q02092 gallus gall |
| 35 | 113.5 | 10.1 | 638  | 1 | GHR_PIG    | P19756 sus scrofa  |
| 36 | 112.5 | 10.0 | 1162 | 1 | LIFR_MOUSE | P48356 mus musculu |
| 37 | 112   | 10.0 | 462  | 1 | IL6A_RAT   | P22273 rattus norv |
| 38 | 112   | 10.0 | 537  | 1 | IL2B_RAT   | P26896 rattus norv |
| 39 | 111.5 | 9.9  | 415  | 1 | IL5R_MOUSE | P21183 mus musculu |
| 40 | 110.5 | 9.9  | 1005 | 1 | EPAS_RAT   | P54757 rattus norv |
| 41 | 109.5 | 9.8  | 507  | 1 | EPOR_MOUSE | P14753 mus musculu |
| 42 | 109   | 9.7  | 420  | 1 | IL5R_HUMAN | Q01344 homo sapien |
| 43 | 108.5 | 9.7  | 551  | 1 | IL2B_HUMAN | P14784 homo sapien |
| 44 | 107.5 | 9.6  | 638  | 1 | GHR_HUMAN  | P10912 homo sapien |
| 45 | 107   | 9.5  | 467  | 1 | IL6A_PIG   | O18796 sus scrofa  |

## ALIGNMENTS

```

RESULT 1
ID IL6B_MOUSE STANDARD; PRT; 917 AA.
AC Q00560;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GPI30).
GN IL6ST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX [1]
NCBI Taxid=10090;
RP SEQUENCE FROM N. A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibl M., Taga T., Kishimoto T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal
RT transducer, gp130, and its regulated expression in vivo.";
RL J. Immunol. 148:4066-4071(1992).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
CC EXCEPT BAR-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
CC CELLS.
CC -!- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
CC DURING THE REST OF EMBRYOGENESIS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, X62646; CAA44515.1; -
DR EMBL, M83336; AAA37723.1; -
DR PIR, I49699; I49699.
DR HSSP, P40189; 1BQV.
DR MGD, MGI:96560; 1166c.
DR GO, GO:0007165; P:signal transduction; IDA.
DR InterPro, IPR002396; CRIA.

```

DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam: PF00041; fn3; 4.  
 DR SMART: SMO0060; FN3; 5.  
 DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;  
 KM Repeat.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.  
 FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 618 639 POTENTIAL.  
 FT DOMAIN 640 917 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 26 120 IG-LIKE C2-TYPE.  
 FT DOMAIN 124 220 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 221 322 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 323 420 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 422 515 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 516 611 FIBRONECTIN TYPE-III 5.  
 FT DOMAIN 723 741 SER-RICH.  
 FT DISULFID 28 54 By similarity.  
 FT DISULFID 48 103 By similarity.  
 FT DISULFID 134 144 By similarity.  
 FT DISULFID 172 180 By similarity.  
 FT DISULFID 456 464 By similarity.  
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 917 AA; 102452 MW; FCEED220BC466F4 CRC64;

Query Match 24.28; Score 271.5; DB 1; Length 917;  
 Best Local Similarity 31.45; Pred. No. 1.6e-17;  
 Matches 66; Conservative 45; Mismatches 84; Indels 15; Gaps 9;

QY 3 PAKPENISCVYYRKNLTCTWSPGKETS-TOYTKVTFVAFGKHNDCTNSSTSENRAS 61  
 DB 126 PDPRNTLTCTVNEGKNMLCQMDPERETVLTNTLTKSEMA-TEKFPDQSGKHGT-----S 179  
 QY 62 CSF-FLPRITPDNYTIEVAENGDAVGIKSMYTWRLNIAKTEPKIFVKEVLGIKRM 120  
 DB 180 CWSYMTYV--NIEVWVAENALGKVSSEINPDVDKVKPTPPVNLVTNSELSST 237  
 QY 121 IQIEWIKPELAPVSSDLKTLRFTNSTSMMEVNFANRKNQYNTLTGLOPFTEYVI 180  
 DB 238 LKLSWSSGGLG-LDKSDIQYRTKASFTWIVPL-EDTMSPTSTFTVODLKPFTEYV 295  
 QY 181 ALRCAYVES--KFMDSQSKMGTEBEAP 208  
 DB 296 RIR-STKDSGKGWSDMSEASGTYEDRP 324

RESULT 2  
 IL6B HUMAN  
 ID IL6B HUMAN STANDARD; PRT; 918 AA.

AC P40189; Q9U041;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) [Interleukin  
 6 signal transducer] (Membrane glycoprotein 130) (GP130) (Oncofostatin M  
 receptor) (CDW130) (CD130 antigen).  
 GN IL6ST.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Myeloma, and Placenta;  
 RX MEDLINE=91084844; PubMed=2261637;  
 RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;  
 RT "Molecular cloning and expression of an IL-6 signal transducer,  
 RT gp130.";  
 RL Cell 63:1149-1157(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX TISSUE=Synovium;  
 RA MEDLINE=20341529; PubMed=10880057;  
 RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,  
 RA Murakami M., Nakao K.;  
 RT "Cloning of novel soluble gp130 and detection of its neutralizing  
 RT autoantibodies in rheumatoid arthritis.";  
 RL J. Clin. Invest. 106:137-144(2000).  
 RN [3]  
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=21269388; PubMed=11098061;  
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;  
 RT "Determination of the disulfide structure and N-glycosylation sites of  
 RT the extracellular domain of the human signal transducer gp130.";  
 RL J. Biol. Chem. 276:8244-8253(2001).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.  
 RX MEDLINE=98169383; PubMed=9501088;  
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;  
 RT "Crystal structure of a cytokine-binding region of gp130.";  
 RL EMBO J. 17:1665-1674(1998).  
 CC -1- FUNCTION: Signal-transducing molecule. The receptor systems for  
 CC IL-6, IL-6, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for  
 CC initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)  
 CC complex, resulting in the formation of high-affinity IL-6 binding  
 CC sites, and transduces the signal. Does not bind IL-6. May have a  
 CC role in embryonic development (By similarity).  
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).  
 CC -1- Secreted (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P40189-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Gp130-RAPs;  
 CC IsoId=P40189-2; Sequence=VSP\_001684;  
 CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines  
 CC examined. Expression not restricted to IL-6 responsive cells.  
 CC -1- DISBASE: Isoform 2 is an autoantigen found in rheumatoid arthritis  
 CC (RA) but it is not specific to patients with RA.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/proc/proc/cd/cd130.htm".  
 CC -----  
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 CC -----  
 DR EMBL; M57230; AAA59155.1; -;  
 DR EMBL; AB015706; BAA78112.1; -;  
 DR PIR; A36337; A36337.  
 DR PDB; 1B0U; 26-AUG-98.  
 DR PDB; 1B08; 13-JAN-99.  
 DR PDB; 1IIR; 28-MAR-01.  
 DR Genew; HGNC:6021; IL6ST.  
 DR MIM; 600694; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004898; F:gp130; TAS.  
 DR GO; GO:0004924; F:oncostatin-M receptor activity; TAS.  
 DR GO; GO:0004872; F:receptor activity; TAS.

|          |  |  |              |     |            |     |        |     |      |     |
|----------|--|--|--------------|-----|------------|-----|--------|-----|------|-----|
|          | Matches  | 66;  | Conservative | 47; | Mismatches | 76; | Indels | 29; | Gaps | 11, |
| Oy       | 3  | PAPENISCYVYRRKALITCWSPEKTSY-QTYVK---RTYAAG---              | KHD--NCTTN   | 52  |            |     |        |     |      |     |
| Dd       | 126  | PERPKNCISCIVNGKKRCCEWGDREHLETFNLTKSEMAHTHKPADCKARDPTSCVD   | 185          |     |            |     |        |     |      |     |
| Oy       | 53   | SSTSENASCSFPLRFTTIDNTLTIEAANGGVICS-HMTYRLRNLIATKEBPKFVR    | 111          |     |            |     |        |     |      |     |
| Dd       | 186  | YST-----VFVV-----NEWWEAEANAIGKTSDIHNPVXKV-KPNPHNISLV       | 230          |     |            |     |        |     |      |     |
| Oy       | 112  | KPVLGIKRMIOIEMKPDELPAVSDDLYTLRFPTNVNSTMWEEVAFAKRDKDQNYLGTG | 171          |     |            |     |        |     |      |     |
| Dd       | 231  | INSELSSILKLWTNSITSVII-LKNYOYRKASTMSQLP-PEDTASTRSSFYOD      | 288          |     |            |     |        |     |      |     |
| Oy       | 172  | LQPFTEYVALRCAYESK-FWSDWGSKOKMTEEAP                         | 208          |     |            |     |        |     |      |     |
| Dd       | 289  | LKPFTEYFRIRCWKGDKGWSDWSEASGITIEDRP                         | 326          |     |            |     |        |     |      |     |
|          | RESULT 3   |  |              |     |            |     |        |     |      |     |
| IL6B_RAT | ID IL6B_RAT STANDARD; PRT; 918 AA.   |  |              |     |            |     |        |     |      |     |
| AC       | P40190;  |  |              |     |            |     |        |     |      |     |
| DT       | 01-FEB-1995 (Rel. 31, Last sequence update)                                |  |              |     |            |     |        |     |      |     |
| DT       | 01-FEB-1995 (Rel. 31, Last sequence update)                                |  |              |     |            |     |        |     |      |     |
| DE       | 16-OCT-2001 (Rel. 40, Last annotation update)                              |  |              |     |            |     |        |     |      |     |
| DE       | Interleukin-6 receptor beta chain precursor (IL-6-beta) [interleukin       |  |              |     |            |     |        |     |      |     |
| DN       | 6 signal transducer] (Membrane glycoprotein I30) (GP130).                  |  |              |     |            |     |        |     |      |     |
| OS       | Rattus norvegicus (Rat).   |  |              |     |            |     |        |     |      |     |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;          |  |              |     |            |     |        |     |      |     |
| OC       | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muriinae; Rattus.     |  |              |     |            |     |        |     |      |     |
| OX       | NCBI_Taxid=10116;  |  |              |     |            |     |        |     |      |     |
| RY       | [1]  |  |              |     |            |     |        |     |      |     |
| RP       | SEQUENCE FROM N.A.   |  |              |     |            |     |        |     |      |     |
| RC       | TISSUE=Liver:  |  |              |     |            |     |        |     |      |     |
| RX       | MEDLINE=93052397; PubMed=1427893;  |  |              |     |            |     |        |     |      |     |
| RA       | Wang Y., Neeshitt J.E., Fuentes N.L., Fuller G.M.;                         |  |              |     |            |     |        |     |      |     |
| RT       | "Molecular cloning and characterization of the rat liver IL-6 signal       |  |              |     |            |     |        |     |      |     |
| RL       | transducing molecule, gp130.";   |  |              |     |            |     |        |     |      |     |
| RT       | Genomics 14:666-672(1992).   |  |              |     |            |     |        |     |      |     |
| CC       | -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR        |  |              |     |            |     |        |     |      |     |
| CC       | IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING           |  |              |     |            |     |        |     |      |     |
| CC       | SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,           |  |              |     |            |     |        |     |      |     |
| CC       | RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,            |  |              |     |            |     |        |     |      |     |
| CC       | AND TRANSDUces THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN          |  |              |     |            |     |        |     |      |     |
| CC       | EMBRYONIC DEVELOPMENT (BY SIMILARITY).                                     |  |              |     |            |     |        |     |      |     |
| CC       | -!- SUBUNIT: Heterodimer of an alpha and a beta chain.                     |  |              |     |            |     |        |     |      |     |
| CC       | -!- SUBCELLULAR LOCATION: Type I membrane protein.                         |  |              |     |            |     |        |     |      |     |
| CC       | -!- TISSUE SPECIFICITY: FOUND IN HEPATOcyTES, ASTROcyTES, FIBROBLASTS      |  |              |     |            |     |        |     |      |     |
| CC       | AND ENDOTHELIAL CELLS.   |  |              |     |            |     |        |     |      |     |
| CC       | -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.             |  |              |     |            |     |        |     |      |     |
| CC       | -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.               |  |              |     |            |     |        |     |      |     |
| CC       | -- --  |  |              |     |            |     |        |     |      |     |
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| CC       | the European Bioinformatics Institute. There are no restrictions on res-   |  |              |     |            |     |        |     |      |     |
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| CC       | or send an email to license@isb-sib.ch).                                   |  |              |     |            |     |        |     |      |     |
| CC       | -- --  |  |              |     |            |     |        |     |      |     |
| DR       | EMBL; M92340.; - NOT_ANNOTATED_CDS.  |  |              |     |            |     |        |     |      |     |
| DR       | PIR; A44257; A44257.   |  |              |     |            |     |        |     |      |     |
| DR       | HSPB; P40189; IBQU.  |  |              |     |            |     |        |     |      |     |
| DR       | InterPro; IPRO02996; CR1A.   |  |              |     |            |     |        |     |      |     |
| DR       | InterPro; IPRO03961; FN II.  |  |              |     |            |     |        |     |      |     |
| DR       | InterPro; IPRO03529; Hemtopoptn_L_Fz.                                      |  |              |     |            |     |        |     |      |     |
| DR       | Ffam; PF00041; fn3; 3.   |  |              |     |            |     |        |     |      |     |
| DR       | SMART; SM00060; FN3; 4.  |  |              |     |            |     |        |     |      |     |
| DR       | PROSITE; PS01353; HEMLTOPO_REC_L_Fz; 1.                                    |  |              |     |            |     |        |     |      |     |
| FW       | Receptor; Transmembrane; Glycopoltein; Immunoglobulin domain; Signal;      |  |              |     |            |     |        |     |      |     |



|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query March           | 17.0%;           | Score 191;         | DB 1;      | Length 608; |
| Best Local Similarity | 27.8%;           | Pred. No. 3.2e-10; |            |             |
| Matches 57;           | Conservative 38; | Mismatches 92;     | Indels 18; | Gaps 10;    |

| RESULT 5      |             |
|---------------|-------------|
| PRLR_COLL1    | STANDARD;   |
| ID_PRLR_COLL1 | PRT; 830 AA |

```

DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Prolactin receptor precursor (PRL-R) .
GN      PRLR.
OS      Columba livia (Domestic pigeon) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX      NCBI_TaxId=8932;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=CropSac;
RX      MEDLINE=94283267; PubMed=7516866;
RA      Chen X., Horsemann N.D.;
RT      "Cloning, expression, and mutational analysis of the pigeon prolactin
RT      receptor".
RL      Endocrinology 135:269-276(1994) .
CC      -I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC      PROLACTIN.
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC      -I- SIMILARITY: Contains 4 fibronectin type III domains.
CC      -----
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|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 17.0%;           | Score 190.5;       | DB 1;      | Length 830; |
| Best Local Similarity | 27.9%;           | Pred. No. 5.3e-10; |            |             |
| Matches 57;           | Conservative 27; | Mismatches 105;    | Indels 15; | Gaps 6;     |

| RESULT 6     |                       |
|--------------|-----------------------|
| PLR CEREL    |                       |
| ID PLR CEREL | STANDARD; PRT; 581 AA |

DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Prolactin receptor precursor (PRL-R).  
GN PRLR.  
OS *Cervus elaphus* (Red deer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
OC Cervidae; Cervinae; Cervus.  
OX NCBI\_TaxID=9860;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=66030711; PubMed=7561644;  
RA Clarke L.A., Boley M., London A.S., Randall V.A., Postal-Vinay M.C.

RA Kelly P.A., Jabbour H.N.;  
 RT "Expression of the prolactin receptor gene during the breeding and  
 RT non-breeding seasons in red deer (*Cervus elaphus*): evidence for the  
 RT expression of two forms in the testis.";  
 RL J. Endocrinol. 146:313-321 (1995).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 CC PROLACTIN.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL: X94953; CA64419.1; -.  
 DR HSPB; P14787; IAN3.  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003961; FN.III.  
 DR InterPro: IPR003528; Hemtopoptn\_L\_FI.  
 DR Pfam; PF00041; FN3; 2.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO REC L\_FI; 1.  
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 PT SIGNAL 1 24  
 FT CHAIN 25 581  
 FT DOMAIN 25 234  
 FT TRANSLEM 235 258  
 FT DOMAIN 259 581  
 FT DOMAIN 25 122  
 FT DOMAIN 123 227  
 FT DISULFID 36 46  
 FT DISULFID 75 86  
 FT CARBOHYD 59 59  
 FT CARBOHYD 132 132  
 FT CARBOHYD 233 233  
 SO SEQUENCE 581 AA; 65159 MW; 975E47CB63CE28BC CRC64;  
 Query Match 16.7%; Score 187; DB 1; Length 581;  
 Best Local Similarity 29.9%; Pred. No. 7.1e-10;  
 Matches 63; Conservative 27; Mismatches 89; Indels 32; Gaps 12;  
 QY 3 PAKPENISCVYYVKNLCTWSPGKENSY--TOYTVKRTY-AFGEX--HDNCTNNSSEN 58  
 DB 28 PGRKXIIKCRSPGKETFTCMWEPESDGLPTNITL--TYHKEGTLIHE--CPDYKTGGPN 84  
 QY 59 RASCSFPLPRTITPDNTIIEVEANGDGVKSHMTYWRLENIAKTEPPKIFRV----- 111  
 DB 85 --TCYFSPKSKHTSIKIKIVITVNAINQGVSSDPLYVDVYIYEPEPAULTELEKPED 142  
 QY 112 -KPTLGKRMIIQIWIPELAPVSSD--LKYTRFTVNSTSMENFPAKRNKQNTY 167  
 DB 143 RKPLMLMK-----WPPPTLTDVSGWFMQYERLRLKPEAADM--EIHFAA-----KOTOL 191  
 QY 168 NLTLGLOPTEYVIALRCVAVESKRWMSQSE 198  
 DB 192 KIRSLYFGQKYLVOVRCK-PDGHGWSMSPE 221  
 RESULT 7  
 PRLR SHEEP STANDARD; PRT; 581 AA.  
 AC O46561; O46569; O46573; O46574; P79203; P79205;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (OPR).  
 GN PRLR.  
 OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_Taxid=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Liver, and Mammary gland;  
 RX MEDLINE=98001468; PubMed=9343303;  
 RA Bignon C., Bihart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;  
 RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
 RT and genomic analysis reveal that the two forms arise by different  
 RT alternative splicing mechanisms in ruminants and in rodents.";  
 RL J. Mol. Endocrinol. 19:109-120 (1997).  
 RN [2]  
 RP SEQUENCE OF 61-395 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE  
 RP SPECIFICITY.  
 RC STRAIN=Scottish blackface; TISSUE=anterior pituitary;  
 RX MEDLINE=99049302; PubMed=9832462;  
 RA Tortorese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;  
 RT "Detection of prolactin receptor gene expression in the sheep  
 RT pituitary gland and visualization of the specific translation of the  
 RT signal in gonadotrophs.";  
 RL Endocrinology 139:5215-5223 (1998).  
 RN [3]  
 RP SEQUENCE OF 147-302 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE  
 RP SPECIFICITY.  
 RC TISSUE=Corpus luteum, and Fetal liver;  
 RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;  
 RT "Two forms of the prolactin receptor messenger ribonucleic acid are  
 RT present in ovine fetal liver and adult ovary.";  
 RL Endocrine 3:291-295 (1995).  
 CC -1- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=Long, L-OPR;  
 CC IsoId=O46561-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short, S-OPR;  
 CC IsoId=O46561-2; Sequence=VSP\_001732, VSP\_001733;  
 CC Name=3; Synonyms=Soluble;  
 CC IsoId=O46561-3; Sequence=VSP\_001730, VSP\_001731;  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined, liver,  
 CC pituitary, adrenal gland, ovary and fetal liver.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL: AF041257; AAB96795.1; -.  
 DR EMBL; AF041977; AAB96920.1; -.  
 DR EMBL; AF041979; AAB97082.1; -.  
 DR EMBL; AF042358; AAB97744.1; -.  
 DR EMBL; AF042358; AAB97743.1; -.  
 DR EMBL; AF041978; AAB96965.1; -.  
 DR EMBL; Y10578; CAA71597.1; -.  
 DR EMBL; Y10808; CAA71766.1; -.  
 DR HSPB; P14787; IAN3.  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003961; FN.III.  
 DR InterPro: IPR003528; Hemtopoptn\_L\_FI.  
 DR Pfam; PF00041; FN3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO REC L\_FI; 1.  
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 GN Alternative splicing.  
 FT SIGNAL 1 24  
 FT SIGNAL 24 POTENTIAL.

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FT CHAIN 25 581 PROACTIN RECEPTOR.
FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 24 66 GOSPPKPLIKRSGKFTGCMWRGADGCPNTYLY
RK -> ASLVPGCKSSVCTTAYVPGVIGTFLMTLCVQD
YLLLVTS (in isoform 3).
FT VARSPPLIC 67 581 /FTId=VSP 001730.
FT VARSPPLIC 286 296 Missing (in isoform 3).
FT VARSPPLIC /FTId=VSP 001731.
FT VARSPPLIC KGSBELRL -> ISQSRSLVSF (in isoform
2).
FT VARSPPLIC /FTId=VSP 001732.
FT VARSPPLIC Missing (in isoform 2).
FT CONFLICT 281 281 /FTId=VSP 001733.
FT CONFLICT I -> V (IN REF. 1; AAB97743/AAB97744).
FT CONFLICT 387 387 E -> K (IN REF. 2).
SQ SEQUENCE 581 AA; 65235 MW; EC534FDE538637A0 CRC64;

Query Match 16.5%; Score 185; DB 1; Length 581;
Best Local Similarity 29.4%; Pred. No. 1.1e-09;
Matches 65; Conservative 27; Mismatches 97; Indels 32; Gaps 12;

QY 3 PAKPENISCVYYRKRLTCTWSPGKETS-YQYTVKRTY-ARGEK-HDNCTNNTSSSEN 58
DB 28 PEKPKIKRSPKPEFTCMWEPGAGGLPTNTL--TYRKEBELTIEH-CPDYKTCGPN 84
QY 59 RASCSFPLPRITIPDNYTIEVEAENGDDGYKSHMTWRLNIAKTEPKIFRY----- 111
DB 85 --SCVSKYKTSIKWKMVITVSAINQMGISSDPLVVDYVYIEPPPNVLTIELGHPED 142
QY 112 -KPVIGIKEMIQIEMIKPELAPVS--DLKYLTRFTVNSTSWMEVNAKNEKDKNQY 167
DB 143 RKRYLMIK-----WSPPLTLDVKSQWPSIQYIEIRLKEPATGW-ETHFA----PLTLQL 191
QY 168 NLGTLOPFEYVIALNCVAVESKFSQWDSQEKMGTEEPAP 208
DB 192 KIFNLVPGQKYLVOIRCK-PDHGYSWSEWSPESFIQIPNDP 231

RESULT 8
ID 112S_HUMAN STANDARD; PRT; 862 AA.
AC Q99665;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-
2) (IL-12R-beta2).
GN IL12RB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; Pubmed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits."
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -1- SUBUNIT: DIMER/OLIGOMER, DISULFIDE-LINKED. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.

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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
-----
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-----
DR EMBL; U64198; AAB36675.1; -.
DR HSSP; P40189; 1BOU.
DR Genew; HGNC:5972; IL12RB2.
DR MIM; 601642; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004907; F:interleukin receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN-III.
DR InterPro; IPR003529; Hemtopopln_L_F2.
DR Pfam; PF00041; FN3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS01353; HEMATOPO REC L_F2; 1.
DR KMW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 862
FT TRANSMEM 625 641
FT DOMAIN 642 862
FT DOMAIN 224 306
FT DOMAIN 421 508
FT DOMAIN 519 607
FT CARBOHYD 48 48
FT CARBOHYD 129 129
FT CARBOHYD 166 166
FT CARBOHYD 195 195
FT CARBOHYD 271 271
FT CARBOHYD 347 347
FT CARBOHYD 376 376
FT CARBOHYD 480 480
FT VARIANT 185
FT VARIANT 420
FT VARIANT 426
FT VARIANT 465
FT FT 465
SQ SEQUENCE 862 AA; 97134 MW; 67C0BD0946B8DD58 CRC64;

Query Match 16.4%; Score 184; DB 1; Length 862;
Best Local Similarity 29.6%; Pred. No. 2.2e-09;
Matches 64; Conservative 28; Mismatches 96; Indels 28; Gaps 10;

QY 3 PAKPENISCVYYRKRLTCTWSPGKETS-YQYTVKRTY-ARGEK-HDNCTNNTSSSENRA 60
DB 124 PEOPNLSCIOEGEAGTACWTERGRDTHLYTEYLQIS--GPK-NLTWQCKCKD-I 176
QY 61 SCSPF-----LPRITIPDNYTIEVEAENGDDGYKSHMTWRLNIAKTEPKIFRYKPV 115
DB 177 YCDYIDDFGINLTPBSPESNFTAKVAVNSLSSSLPSTFTLDVRLPPLPDITIKRK 236
QY 116 GIKRMIOIEMIKPELAPVSSDLKYLTRFTVNSTSWMEVNF-AKRRDKQNTYVLTGLQ 173
DB 237 ASVSRCTIYWRDEGLV-----LNLRLRYRPSNSRLMNVNVTYKAKGRD-----L 285
QY 174 PTEYVIALRCVAVESK-FWSDWSQEKMGTEEPAP 208
DB 286 PTEYEFQIISKRLILYKGSWDSSESRLRAQPTPEEP 321

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RESULT 9
PRLR_BOVIN STANDARD; PRT; 581 AA.
ID Q28172; 018880; 046591;
AC Q28172; 018880; 046591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RN RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Endometrium;
RX MEDLINE=93246019; PubMed=1338725;
RA Scott P., Kessler M.A., Schuler L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
RT of prolactin and growth hormone receptor transcripts in fetal and
RT utero-placental tissues."
RL Mol. Cell. Endocrinol. 89:47-58(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY.
RC TISSUE=Endometrium;
RX MEDLINE=9375450; PubMed=9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues."
RL Endocrinology 138:3187-3194(1997).
RN [3]
RP SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.
RC TISSUE=Mammary gland;
RX MEDLINE=95256770; PubMed=7738463;
RA Thelet A., Statten N.R., Creely D.P., Krivi G.G., Gertler A.;
RT "Extracellular domain of prolactin receptor from bovine mammary gland:
RT expression in Escherichia coli, purification and characterization of
RT its interaction with lactogenic hormones."
RL J. Endocrinol. 144:393-403(1995).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=98001468; PubMed=9343303;
RA Blynon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Diane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
RT and genomic analysis reveal that the two forms arise by different
RT alternative splicing mechanisms in ruminants and in rodents."
RL J. Mol. Endocrinol. 19:109-120(1997).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q28172-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q28172-2; Sequence=VSP 001718, VSP 001719;
CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,
CC peripheral blood lymphocytes, endometrium, corpus luteum,
CC intestine, fetal thymus, fetal spleen, fetal liver and fetal
CC brain.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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DR EMBL; L02549; AAA51417.1; -.
DR EMBL; AF027403; AAB83999.1; -.
DR EMBL; AF042780; AAB97748.1; -.
DR EMBL; AF042780; AAB97747.1; ALT_SEQ.
DR PIR; I45971; I45971.
DR HSSP; P14787; IAN3.
DR InterPro; IPR002996; CRA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PR00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT VARSPLIC 266 296
FT FT VARSPLIC 297 581
FT FT VARSPLIC 120 120
FT FT CONFLICT 128 128
FT FT CONFLICT 137 137
FT FT CONFLICT 141 141
FT FT CONFLICT 156 157
FT FT CONFLICT 186 186
SQ SEQUENCE 581 AA; 65153 MW; 7385CD0695EBE139 CRC64;
Query Match 16.3%; Score 183; DB 1; Length 581;
Best Local Similarity 28.9%; Pred. No. 1.7e-09;
Matches 61; Conservative 28; Mismatches 90; Indels 32; Gaps 12;
QY 3 PAKPENISCVYYRRKRLTCTWSPGKETS-TOYIVKRY-ARGEK--HNDCTNSTSEN 58
DB 28 PEKPKLVKRSRSGKEFTCWMEPGADGLPTVYTL--TYHKGERTLIHE-CPDYKYGPN 84
QY 59 RASGCFELPRITIPDNYTTEVAENGQGYKSHMTYRLLENIAKTEPKIFRY----- 111
DB 85 --SCVFSKGTSTIMKRYVITVNAINQMGISSSDPLYVHTYIVVEPPPNLTLLEKHPD 142
QY 112 -KPVGIKRMIGIEMIKPELAVSSD--LKYTLRPRTVNSTSWMEVNFARKKDKNQTY 167
DB 143 KPEYLMIK-----MSPTMTDVKSGWFIQYRIKPEKAYDW-ETHTTL-----KOTOL 191
QY 168 NLGLOPFTFYIALRCAYVSKSFWSWSQE 198
DB 192 KIFNLYPGQKYLVIQIRCK-PDHGYWSEWSPE 221
RESULT 10
PRLR_RAT STANDARD; PRT; 610 AA.
ID P05710; 062832; 063451; 063479; 063723; 064274;
AC P05710; 062832; 063451; 063479; 063723; 064274;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (Lactogen receptor).
GN PRLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]

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RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=91155946; PubMed=2293022;  
 RA Shirota M., Banville D., Ali S., Jolicoeur C., Boutin J.M.,  
 RA Edey M., Djiane J., Kelly P.A.;  
 RT "Expression of two forms of prolactin receptor in rat ovary and  
 RT liver";  
 RL Mol. Endocrinol. 4:1136-1143(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
 RX MEDLINE=90241201; PubMed=2159291;  
 RA Zhang R., Buckco E., Tsai-Morris C.-H., Hu Z.Z., Dufau M.L.;  
 RT "Isolation and characterization of two novel rat ovarian laccogen  
 RT receptor cDNA species";  
 RL Biochem. Biophys. Res. Commun. 168:415-422(1990).  
 RN [3]  
 RP SEQUENCE OF 281-610 FROM N.A.  
 RA Banville D., Stocco R., Murthy K.K., Boie Y., Kelly P.A.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=88165059; PubMed=2832068;  
 RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Edey M.,  
 RA Shirota M., Banville D., Dusanter-Pourt I., Djiane J., Kelly P.A.;  
 RT "Cloning and expression of the rat prolactin receptor, a member of  
 RT the growth hormone/prolactin receptor gene family";  
 RL Cell 53:69-77(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RC TISSUE=Lymphoma;  
 RX MEDLINE=92041834; PubMed=1718958;  
 RA Ali S., Pelligrini I., Kelly P.A.;  
 RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form  
 RT of prolactin receptor";  
 RL J. Biol. Chem. 266:20110-20117(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RX MEDLINE=95014432; PubMed=7929319;  
 RA O'Neal K.D., Yu-Lee L.Y.;  
 RT "Differential signal transduction of the short, Nb2, and long  
 RT prolactin receptors. Activation of interferon regulatory factor-1 and  
 RT cell proliferation";  
 RL J. Biol. Chem. 269:26076-26082(1994).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 CC PROLACTIN.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Long;  
 CC IsoId=P05710-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=P05710-2; Sequence=VSP\_001725, VSP\_001726;  
 CC Name=3; Synonyms=Medium;  
 CC IsoId=P05710-3; Sequence=VSP\_001727, VSP\_001728;  
 CC Name=4; Synonyms=NB2;  
 CC IsoId=P05710-4; Sequence=VSP\_001729;  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL; M57688; AAA41938.1; -  
 CC EMBL; M34083; AAA79273.1; -  
 CC EMBL; I48060; AAA79274.1; -  
 CC EMBL; U34730; AAA92053.1; -  
 CC EMBL; M19304; AAA41937.1; -  
 CC DR

DR EMBL; M74152; AAA41946.1; -  
 DR EMBL; U07567; AAA61784.1; -  
 DR PIR; A29884; A29884.  
 DR PIR; A34631; A34631.  
 DR PIR; A36116; A36116.  
 DR PIR; A41070; A41070.  
 DR PIR; B34631; B34631.  
 DR PDB; 1F6F; 20-DEC-00.  
 DR InterPro; IPR002396; CR1A.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR003528; Hemtopopn\_L\_F1.  
 DR Pfam; PF00041; FN3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO RECL\_F1; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1  
 FT CHAIN 19  
 FT DOMAIN 20 610  
 FT TRANSMEM 20 229  
 FT DOMAIN 230 253  
 FT DOMAIN 254 610  
 FT DOMAIN 20 117  
 FT DOMAIN 119 222  
 FT DISULFID 31 41  
 FT DISULFID 70 81  
 FT CARBOHYD 54 54  
 FT CARBOHYD 99 99  
 FT CARBOHYD 127 127  
 FT VARSPLIC 131 150  
 FT VARSPLIC 151 610  
 FT VARSPLIC 281 310  
 FT VARSPLIC 311 610  
 FT VARSPLIC 342 539  
 FT CONFLICT 236 236  
 FT CONFLICT 345 345  
 FT CONFLICT 465 465  
 FT CONFLICT 466 466  
 FT CONFLICT 469 469  
 FT CONFLICT 541 541  
 FT CONFLICT 555 555  
 SQ SEQUENCE 610 AA; 68599 MW; 83D04D832861295D CRC64;  
 Query Match 16.1%; Score 181; DB 1; Length 610;  
 Best Local Similarity 27.9%; Pred. No. 2.8e-09;  
 Matches 57; Conservative 35; Mismatches 94; Indels 18; Gaps 10;  
 QY 3 PAKPENISCVYYRRNLTCTWSPGKETS-YTQYVKTYYA-FGEKRD-NCTNSTSENK 59  
 DB 23 PCKPEIHRCRSPDKTFPCWNNPGLDGLPYNYSL-TYSKGEKTYTECPDYKSGN- 79  
 QY 60 ASCSFLRITIPDNYTEVAENGDVYKSHMTYRLENIAKTEPK--IFRYVPVGLI 117  
 DB 80 -SCFSSKOYTSIMWKYIITVNAIYQMGSSDPLVDVDTYIVPEPPNLTLEVAQLDK 138  
 QY 118 KRMIDIEIKPELAPVSS--DLKTYLFRFVNSTSNMENVPAKRRKXKXQNYNLGLOP 174  
 DB 139 KTYLWKKSPPIITDVKTGWMTEYELKBEAEEM-EIHFTGHQTO---FKVPDLXP 193  
 QY 175 FTEYVIALCAVKSKEKSWDSOE 198  
 DB 194 GQKYLIVQTRCK-PDHGYWRSWSOE 216  
 RESULT 11  
 PRIR CHICK  
 ID PRIR CHICK STANDARD; PRT; 831 AA.

AC 004594; (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE prolactin receptor precursor (PRL-R) (CPLP).  
GN PRLR.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White Leghorn; TISSUE=kidney;  
RX MEDLINE=93075121; PubMed=1445292;  
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;  
RT "Double antenna structure of chicken prolactin receptor deduced from  
the cDNA sequence.";  
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
PROLACTIN.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; D13154; BAA02439.1; -.  
DR PTR; J01655; J01655.  
DR HSSP; P16471; 1BB3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003528; Hemtopopcn\_L\_F1.  
DR Pfam; PF00041; fn3; 4.  
DR SMART; SMO0060; FN3; 3.  
DR PROSITE; PS01352; HEMATOPO\_RBC\_L\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 831 PROLACTIN RECEPTOR.  
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 439 459 POTENTIAL.  
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 75 86 BY SIMILARITY.  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 831 AA; 94102 MW; 1CAE75791DCADBE9 CRC64;

|                       |       |                   |      |                |
|-----------------------|-------|-------------------|------|----------------|
| Query Match           | 16.0% | Score 179.5       | DB 1 | Length 831     |
| Best Local Similarity | 26.7% | Pred. No. 5.7e-09 |      |                |
| Matches               | 54    | Conservative      | 26   | Mismatches 109 |
|                       |       |                   |      | Indels 13      |
|                       |       |                   |      | Gaps 5         |

QY 3 PAKENISCVVYYRKNLTCTWSPKETS-TQYVVKRTAFGEHNDCTNNSSENAS 61  
| | | | |  
| : | | | : | :  
Db 231 PEKTI IKRSPEKETFTCWMKPGIDGGHTNTYLLYSSEGEBOVECDPYRAGPN--S 288

Qy 62 CSEFLRIRIIPDNYLTLEVAENGDSVISHNTYRLENIAKTEPP---KIRVNPVYGIKR 119

Db 289 CYEDKHTSFMTIYITVATATMEKSNSSDPHYADVITYIYVDPDPNAVLTLELKKPINRKP 348

Qy 120 MIDIEWIKBELAPVSS---DLKYTLRPRVTANSTGSMVEVNAKORKDNGTYNLTLGLOPFT 176

Db 349 YLVLTISPPPLDVAISGWLTEYLEIRLKPPEGGEEMETIIPVGOQOTQ----YKPSLNPK 403

Qy 177 EYVIALRCVAKESKFEWDSMOE 198

Db 404 KYIIQIHCKPRDHGSMSEWSE 425

|          | RESULT 12  |           |             |
|----------|------------|-----------|-------------|
| ID       | PRLR MELGA | STANDARD; | PRT; 831 AA |
| 00000000 | 00000000   | 00000000  | 00000000    |

DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 15-JUL-1999 (Rel. 38, last annotation update)  
DE Prolactin receptor precursor (PRL-R) (TPRLR)  
..

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris  
OX NCBI\_TaxID=9103;

RC TISSUE=Kidney;  
RX MEDLINE=97057891; PubMed=8902221;  
RA Zhou J.F., Zadworny D., Glemene D., Kuhnlein U.;

RT gallopavo."?  
RL Biol. Reprod. 55:1081-1090(1996).  
RN [2]

RA Pites G.R., You S.K., Foster D.N., el Halawani M.E.;  
 Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS  
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -----  
CC -----

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CC modified and this statement is not removed. Usage by and for commercial

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CC -----
DR EMBL; L76587; AAB01544.1; -.
DR EMBL; U22947; AAA75038.1; -.

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DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1

| DR | PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.               |
|----|---|
| KM | Receptor; Transmembrane; Glycoprotein; Signal; Repeat |
| FT | SIGNAL 1 23 POTENTIAL.                                |

|    |          |     |     |                          |
|----|----------|-----|-----|--------------------------|
| FT | TRANSMEM | 439 | 459 | POTENTIAL.               |
| FT | DOMAIN   | 460 | 831 | CYTOPLASMIC (POTENTIAL). |
| FT | DOMAIN   | 25  | 122 | FIBRONECTIN TYPE-III 1.  |

FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 831 AA; 94394 MW; 22091632077FAC1 CRC64;  
Query Match 15.7%; Score 176.5; DB 1; Length 831;  
Best Local Similarity 26.2%; Pred. No. 1.1e-08;  
Matches 53; Conservative 26; Mismatches 110; Indels 13; Gaps 5;  
QY 3 PAKPENISCVYYRRKLTCTWSPGKETS-YQYVKTATYAFGRKDNCTTSSSENRA 61  
DB 231 PEKPTITKCRSPEKEFTCMWKPGDLGHPYVTLILYSKEGEQVYECDFRTAGPN--S 288  
QY 62 CSFPLPRITIPDNYTIEVAENGDDGYIKSHMTYMLAKTEPK--IFRYKPVLGIR 119  
DB 289 CYFDKHTSFWTYNTYVATNEMGSSDPHYVDTYIVDPDPANVTLEKKPINRKP 348  
QY 120 MIOIEMIKPELAPVSS--DLKYTLRFRTVNSTSWMEVPAKRNKDKNTYLTGLQPT 176  
DB 349 YLMLTWSPPLADVNSGMLTLDYELKPEEGEWEVTVGQGTQ----YKMFSLNPK 403  
QY 177 EYVIALRCVAKESKFWSDWSOE 198  
DB 404 KYIVQHCXKPDHHSSEWSSE 425  
RESULT 13  
ID 112S MOUSE STANDARD; PRT; 874 AA.  
AC P97378;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).  
GN IL12RB2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97098510; PubMed=8943050;  
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,  
RA Gately M.K., Gubler U.;  
RT "A functional interleukin 12 receptor complex is composed of two  
RT beta-type cytokine receptor subunits";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).  
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A  
CC LOW AFFINITY.  
CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH  
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND  
CC IL12RB2.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL: U64199; AAB36676.1; -  
DR MGI: 1270861; 1112rb2.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hemtopopen\_L\_F2.  
DR Pfam: PF00041; fn3; 4.  
DR SMART: SMO0060; FN3; 4.  
DR PROSITE: PS01353; HEMATOPO. REC. L. F2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 20  
FT CHAIN 1 874  
FT DOMAIN 21 639 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.  
FT TRANSMEM 640 656 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 657 874 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 137 230 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 240 322 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 436 523 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 534 622 FIBRONECTIN TYPE-III 4.  
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 112 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 279 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 874 AA; 98196 MW; 582E4D21B1FBD67 CRC64;  
Query Match 15.6%; Score 174.5; DB 1; Length 874;  
Best Local Similarity 30.8%; Pred. No. 1.1e-08;  
Matches 66; Conservative 31; Mismatches 96; Indels 21; Gaps 11;  
QY 3 PAKPENISCVYYRRKLTCTWSPGKETS-YQYVKTATYAFGRKDNCTTSSSENRA 60  
DB 137 PEKPTITKCRSPEKEFTCMWKPGDLGHPYVTLILYSKEGEQVYECDFRTAGPN--S 288  
QY 62 CSFPLPRITIPDNYTIEVAENGDDGYIKSHMTYMLAKTEPK--IFRYKPVLGIR 119  
DB 289 CYFDKHTSFWTYNTYVATNEMGSSDPHYVDTYIVDPDPANVTLEKKPINRKP 348  
QY 120 MIOIEMIKPELAPVSS--DLKYTLRFRTVNSTSWMEVPAKRNKDKNTYLTGLQPT 176  
DB 349 YLMLTWSPPLADVNSGMLTLDYELKPEEGEWEVTVGQGTQ----YKMFSLNPK 403  
QY 177 EYVIALRCVAKESKFWSDWSOE 198  
DB 404 KYIVQHCXKPDHHSSEWSSE 425  
RESULT 14  
ID PRLR\_RABIT STANDARD; PRT; 616 AA.  
AC P14787;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Prolactin receptor precursor (PRL-R).  
GN PRLR.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP TISSUE=Mammary gland;  
RX MEDLINE=89184578; PubMed=2928321;

RA Edey M., Jolicoeur C., Levi-Meyrueis C., Dusanter-Fourt I.,  
 RA Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;  
 RA "Identification and sequence analysis of a second form of prolactin  
 RT receptor by molecular cloning of complementary DNA from rabbit  
 RT mammary gland."; Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).  
 RN [2]  
 RP 3D-STRUCTURE MODELING OF 30-228.  
 RX MEDLINE=97248733; PubMed=9094747;  
 RA Helaby D., Thoreau E., Djiane J., Mornon J.-P.;  
 RT "homology modeling of rabbit prolactin hormone complexed with its  
 RT receptor."; Proteins 27:459-468(1997).  
 RL Proteins 27:459-468(1997).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 CC PROLACTIN.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: J04510; AAA31457.1; -.  
 DR PIR: A30304; A30304.  
 DR PDB: 1AN3; 03-DEC-97.  
 DR InterPro: IPR002996; CR1A.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR003528; Hemicoptn\_L\_F1.  
 DR Pfam: PF00041; fn3; 2.  
 DR SMART: SM00060; FN3; 2.  
 DR PROSITE: PS01352; HEMITOPD\_REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.  
 FT STGNL 1 24  
 FT CHAIN 25 616  
 FT DOMAIN 25 234 PROLACTIN RECEPTOR.  
 FT TRANSEM 235 258 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III 1.  
 FT DISULFID 36 46 FIBRONECTIN TYPE-III 2.  
 FT DISULFID 75 86 BY SIMILARITY.  
 FT CARBOHYD 59 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT STRAND 36 38  
 FT STRAND 44 46  
 FT STRAND 50 50  
 FT STRAND 55 55  
 FT STRAND 61 65  
 FT STRAND 73 74  
 FT STRAND 77 77  
 FT TURN 83 84  
 FT TURN 86 88  
 FT TURN 91 92  
 FT TURN 98 104  
 FT TURN 109 110  
 FT STRAND 118 120  
 FT TURN 121 124  
 FT STRAND 125 125  
 FT STRAND 131 137  
 FT STRAND 147 152  
 FT TURN 160 161  
 FT STRAND 167 174  
 FT STRAND 181 182  
 FT STRAND 186 186  
 FT STRAND 190 193  
 FT TURN 198 199  
 FT STRAND 202 209

FT STRAND 222 223  
 SQ SEQUENCE 616 AA; 68840 MW; 800E316FEF7108C CRC64;  
 Query Match 15.1%; Score 169; DB 1; Length 616;  
 Best Local Similarity 29.3%; Pred. No. 3,7e-08;  
 Matches 60; Conservative 27; Mismatches 98; Indels 20; Gaps 11;  
 QY 3 PAKPENISCVYYRKNLTCTWSPGKETSY-TQYVARY-ARGE-KHDNCTNSSTSEN 58  
 DB 28 PKRPFIFKRSPEKEFTWWRPGADGLPTVTL--TYHKGFTITHE-CPDYKCGPN 84  
 QY 59 RASCSFELPRITIPDNYITEVAENGQVYKSHMTYRIENIAKTEPP-KIFRYKPVLG 116  
 DB 85 --SCYFSKKHTSIWTYIITVNATNQMGSSVSDPRVDYTVIEBPPVNLTLVGHPEP 142  
 QY 117 IKRMQIEMIKPELAPVVS---DLKYLRFRTVNSWMEVFAKRNKQNTYNTGLQ 173  
 DB 143 KRPYLWVKPLPTLVDVRSGLTLQYEIRLKEPKAEW-ETHPA---GQQTQFKILSLY 197  
 QY 174 PFEVYIALRCVAKSKFWSWSQ 198  
 DB 198 PGKXIVQVRCK-PDHGFWSVSP 221  
 RESULT 15  
 ID GCSR HUMAN STANDARD; PRT; 836 AA.  
 AC 099062;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-FEB-2003 (Rel. 42, Last annotation update)  
 DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)  
 DE (CD114 antigen).  
 GN CSF3R OR GCSFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=91079757; PubMed=2147944;  
 RA Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosman D.,  
 RA Park L., Sorensen E., March C.J., Smith C.A.;  
 RT "Expression cloning of a human granulocyte colony-stimulating factor  
 RT receptor: a structural mosaic of hematopoietin receptors";  
 RT immunoglobulin, and fibronectin domains."; J. Exp. Med. 172:1559-1570(1990).  
 RL J. Exp. Med. 172:1559-1570(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=91062348; PubMed=1701053;  
 RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;  
 RT "Three different mRNAs encoding human granulocyte colony-stimulating  
 RT factor receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=92091782; PubMed=1530796;  
 RA Seto Y., Fukunaga R., Nagata S.;  
 RT "Chromosomal gene organization of the human granulocyte colony-  
 RT stimulating factor receptor."; J. Immunol. 148:259-266(1992).  
 RL J. Immunol. 148:259-266(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANTS THR-231; ASN-320; ARG-346; LYS-405;  
 RP GLN-440; HIS-510; HIS-562 AND CYS-583.  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
 RL Submitted (SEP-2002) to the EMBL/Genbank/DDJJ databases.  
 RN [5]  
 RP DOMAINS STRUCTURE.  
 RX MEDLINE=92007729; PubMed=1717255;  
 RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;

RT "Functional domains of the granulocyte colony-stimulating factor  
RT receptor.";

RL EMOB J. 10:2855-2865(1991).

RN [6]

RP DISEASE.

RX MEDLINE=94240159; PubMed=7514305;

RA Dong F., Hoelsloot L.H., Schellen A.M., Broeders C.A., Meijer Y.,  
RA Veerman A.J., Touw I.P., Lowenberg B.;

RT "Identification of a nonsense mutation in the granulocyte-colony-  
RT stimulating factor receptor in severe congenital neutropenia.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:4480-4484(1994).

RN [7]

RP STRUCTURE BY NMR OF 227-334.

RA MEDLINE=97331327; PubMed=9187659;

RA Yanasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;

RT "Solution structure of an extracellular domain containing the WSXWS  
RT motif of the granulocyte colony-stimulating factor receptor and its  
RT interaction with ligand.";

RL Nat. Struct. Biol. 4:498-503(1997).

RN [8]

RP 3D-STRUCTURE MODELING OF 125-331.

RX MEDLINE=98037802; PubMed=9368043;

RA Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;

RT "Identification of a ligand-binding site on the granulocyte colony-  
RT stimulating factor receptor by molecular modeling and mutagenesis.";

RL J. Biol. Chem. 272:29735-29741(1997).

CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-  
CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION  
CC EVENTS AT THE CELL SURFACE.

CC -1- SUBUNIT: DIMER (PROBABLE).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,  
CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM  
CC OF THE RECEPTOR.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative applying: Named isoforms=4;  
CC Comment-Additional isoforms seem to exist. Experimental  
CC confirmation may be lacking for some isoforms;

CC Name=1; Synonyms=GCSFR-1;  
CC IsoId=Q99062-1; Sequence=Displayed;  
CC Name=2; Synonyms=GCSFR-2;  
CC IsoId=Q99062-2; Sequence=VSP\_001674;  
CC Name=3; Synonyms=GCSFR-3;  
CC IsoId=Q99062-3; Sequence=VSP\_001673;  
CC Name=4; Synonyms=GCSFR-4, D7;  
CC IsoId=Q99062-4; Sequence=VSP\_001671, VSP\_001672;  
CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN  
CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN  
CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.  
CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE  
CC GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

CC -1- DISEASE: Defects in GCSFR might be a cause of severe congenital  
CC neutropenia (SCN) in some patients.

CC -1- SIMILARITY: Contains 5 fibronectin type III domains.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD114 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".

CC -----

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CC -----

DR EMBL; X55721; CAA39253.1; -

DR EMBL; X55720; CAA39252.1; -

DR EMBL; S71484; AAB20660.1; -

DR EMBL; M59818; AAA63176.1; -

DR EMBL; M59819; AAA63177.1; -

DR EMBL; M59820; AAA63178.1; -

DR EMBL; AY148100; AAN05790.1; -

[illegible]

FT VARIANT 562 562 Y -> H.  
FT VARIANT 583 583 /FTid=VAR\_014331.  
FT STRAND 127 133 R -> C.  
FT TURN 135 136 /FTid=VAR\_014332.  
FT STRAND 140 145

Query Match 14.8%; Score 166; DB 1; Length 836;  
Best Local Similarity 27.1%; Pred. No. 1e-07;  
Matches 64; Conservative 22; Mismatches 96; Indels 54; Gaps 10;

QY 3 PAKPENISCVYYRKNLT-----CTWSPGKETSY-TQYTVKRTYAFGEKHNDCTNSST- 55  
Db 123 PAIPHNLSCL-----MNLTSLSLICOEPEGPETHLPISFTLSPKSRG---NCOTQDST 174  
QY 56 -----SENBRASCFFLPRTITIPNDYITEVEAENGSGVTKSHMTYWRLENIAKTEPPKIFR 110  
Db 175 LDCVPRKDGSHCCIPRHLLLYQNGIWOAENALGTSMSPOLCLDPMDVVKLEPPMLRT 234  
QY 111 VKPVLGIKRMIOIEWIKPELAPVSS-----DLKYTLRFRTV-NSTSWME 153  
Db 235 MDP-----SPEAAPPOAGCLQLCWEPWOPGLHINOKCELHKKPORGASWAL 281  
QY 154 VNPANRKNQNYNLTLGLOPTEYVIALRC-AVKESKFWSDWSQEKMGTEEEAP 208  
Db 282 VG---PLPLEALQYELGGLPATAYTLQIRCIHWPLFGHWSWSPSLERLTERAP 334

Search completed: August 18, 2003, 13:27:39  
Job time : 16.81 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:47 ; Search time 73.6152 Seconds  
(without alignments)  
729.128 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_20\_227

Perfect score: 1121  
Sequence: 1 ALPAPENISCVYRRKUL.....SKFMSDWSQEKMGTEBPAP 208

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SP archaea:\*
- 2: SP bacteria:\*
- 3: SP fungi:\*
- 4: SP human:\*
- 5: SP invertebrate:\*
- 6: SP mammal:\*
- 7: SP mhc:\*
- 8: SP organelle:\*
- 9: SP phage:\*
- 10: SP plant:\*
- 11: SP rodent:\*
- 12: SP virus:\*
- 13: SP vertebrate:\*
- 14: SP unclassified:\*
- 15: SP viirus:\*
- 16: SP bacteriap:\*
- 17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 1121  | 100.0       | 509    | 4 Q8WYJ0  | Q8WYJ0 homo sapien |
| 2          | 1121  | 100.0       | 732    | 4 Q8N117  | Q8N117 homo sapien |
| 3          | 502.5 | 44.8        | 716    | 11 Q8K5B1 | Q8K5B1 mus musculu |
| 4          | 502.5 | 44.8        | 716    | 11 Q8K5B1 | Q8K5B1 mus musculu |
| 5          | 287   | 25.6        | 881    | 13 Q57519 | Q57519 xenopus lae |
| 6          | 278   | 24.8        | 918    | 13 Q9W6U9 | Q9W6U9 gallus gall |
| 7          | 231   | 20.6        | 422    | 4 Q9UH55  | Q9UH55 homo sapien |
| 8          | 231   | 20.6        | 422    | 4 Q75462  | Q75462 homo sapien |
| 9          | 229   | 20.4        | 425    | 11 Q9UM58 | Q9UM58 mus musculu |
| 10         | 209   | 18.6        | 861    | 6 Q9BEG2  | Q9BEG2 bos taurus  |
| 11         | 204   | 18.2        | 710    | 13 Q57520 | Q57520 xenopus lae |
| 12         | 203   | 18.1        | 848    | 6 Q8WJ24  | Q8WJ24 sus scrofa  |
| 13         | 198   | 17.7        | 861    | 6 Q8WJ24  | Q8WJ24 sus scrofa  |
| 14         | 194   | 17.3        | 292    | 11 Q8C7G1 | Q8C7G1 mus musculu |
| 15         | 191   | 17.0        | 608    | 11 Q9J0Z1 | Q9J0Z1 mus musculu |
| 16         | 178.5 | 15.9        | 626    | 13 Q90WG7 | Q90WG7 cynops pyr  |

|    |       |      |      |           |                     |
|----|-------|------|------|-----------|---------------------|
| 17 | 172.5 | 15.4 | 604  | 13 Q8Q554 | Q8Q554 cyprinus ca  |
| 18 | 172   | 15.3 | 622  | 6 Q9GLW3  | Q9GLW3 ursus marit  |
| 19 | 169   | 15.1 | 627  | 6 Q9N0J7  | Q9N0J7 callithrix   |
| 20 | 165.5 | 14.8 | 611  | 13 Q9PTB9 | Q9PTB9 xenopus lae  |
| 21 | 162   | 14.5 | 644  | 11 Q8K4B4 | Q8K4B4 mus musculu  |
| 22 | 160   | 14.3 | 629  | 4 Q8WFO9  | Q8WFO9 mus sapien   |
| 23 | 158.5 | 14.1 | 1093 | 11 Q70535 | Q70535 ratus norv   |
| 24 | 156   | 13.9 | 383  | 11 Q88786 | Q88786 mus musculu  |
| 25 | 156   | 13.9 | 385  | 11 Q8VHK6 | Q8VHK6 rattus norv  |
| 26 | 154.5 | 13.8 | 600  | 13 Q9PTP0 | Q9PTP0 carassius a  |
| 27 | 154   | 13.7 | 345  | 13 Q93404 | Q93404 oreochromis  |
| 28 | 154   | 13.7 | 625  | 6 Q9XS92  | Q9XS92 trichosturus |
| 29 | 153.5 | 13.7 | 424  | 11 Q8C123 | Q8C123 mus musculu  |
| 30 | 153   | 13.6 | 206  | 4 Q16354  | Q16354 homo sapien  |
| 31 | 153   | 13.6 | 268  | 4 Q8TD78  | Q8TD78 homo sapien  |
| 32 | 153   | 13.6 | 288  | 4 Q96P36  | Q96P36 homo sapien  |
| 33 | 153   | 13.6 | 349  | 4 Q9UH55  | Q9UH55 homo sapien  |
| 34 | 153   | 13.6 | 376  | 4 Q96P35  | Q96P35 homo sapien  |
| 35 | 151.5 | 13.5 | 212  | 13 Q8JFT3 | Q8JFT3 brachydanto  |
| 36 | 149.5 | 13.3 | 424  | 11 Q8BNM4 | Q8BNM4 mus musculu  |
| 37 | 148.5 | 13.2 | 611  | 13 Q9IBP6 | Q9IBP6 xenopus lae  |
| 38 | 148.5 | 13.2 | 611  | 13 Q9PTI0 | Q9PTI0 xenopus lae  |
| 39 | 146.5 | 13.1 | 372  | 11 Q88507 | Q88507 mus musculu  |
| 40 | 146.5 | 13.1 | 432  | 11 P70225 | P70225 mus musculu  |
| 41 | 145   | 12.9 | 217  | 6 Q46386  | Q46386 mustela vis  |
| 42 | 144   | 12.8 | 109  | 6 Q8SPV0  | Q8SPV0 canis famil  |
| 43 | 142   | 12.7 | 422  | 4 Q16542  | Q16542 homo sapien  |
| 44 | 141.5 | 12.6 | 636  | 13 Q90Z16 | Q90Z16 parallchchy  |
| 45 | 140.5 | 12.5 | 432  | 11 Q64385 | Q64385 mus musculu  |

ALIGNMENTS

| RESULT 1                  | Q8WYJ0  | PRELIMINARY: | PRT: | 509 AA.            |
|---------------------------|---|--------------|------|--------------------|
| AC                        | Q8WYJ0  |              |      |                    |
| DT                        | 01-MAR-2002 (TREMBLrel. 20, Created)                              |              |      |                    |
| DT                        | 01-MAR-2002 (TREMBLrel. 20, Last sequence update)                 |              |      |                    |
| DT                        | 01-JUN-2002 (TREMBLrel. 21, Last annotation update)               |              |      |                    |
| DE                        | CRL3 protein.   |              |      |                    |
| GN                        | CRL3.   |              |      |                    |
| OS                        | Homo sapiens (Human).   |              |      |                    |
| OC                        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |              |      |                    |
| OC                        | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.         |              |      |                    |
| OX                        | NCBI_TaxID=9606;  |              |      |                    |
| RN                        | [1]   |              |      |                    |
| RP                        | SEQUENCE FROM N.A.  |              |      |                    |
| RA                        | Zhang W., Wan T., He L., Yuan Z., Cao X.;                         |              |      |                    |
| RT                        | "A novel soluble type I cytokine receptor."                       |              |      |                    |
| RL                        | Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.           |              |      |                    |
| DR                        | EMBL; AF106913; AAL36452.1; ..                                    |              |      |                    |
| DR                        | InterPro; IPR002996; CRLA.  |              |      |                    |
| DR                        | InterPro; IPR003961; FN_III.                                      |              |      |                    |
| DR                        | Pfam; PF00041; fn3; 2.  |              |      |                    |
| DR                        | SMART; SM00060; FN3; 3.   |              |      |                    |
| SO                        | SEQUENCE 509 AA; 58390 MW; 5DC85C59E170D44B CRC64;                |              |      |                    |
| Query Match               | 100.0%; Score 1121; DB 4; Length 509;                             |              |      |                    |
| Best Local Similarity     | 100.0%; Pred. No. 5,5e-98;  |              |      |                    |
| Matches 208; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;                                |              |      |                    |
| QY                        | 1 ALPAPENISCVYRRKULCTWSGKETSQYTVKRTYVAGRGHNDCTNNTSSSENA 60        |              |      | Q8G54 cyprinus ca  |
| QY                        | 33 ALPAPENISCVYRRKULCTWSPGKETSQYTVKRTYVAGRGHNDCTNNTSSSENA 92      |              |      | Q9G1W3 ursus marit |
| QY                        | 61 SCSPFLPRTTPDNTTIEVEAENGGVKSHMTYRLLENIAKTEBPXIFRYVPGVIGIRM 120  |              |      | Q9N0J7 callithrix  |
| QY                        | 93 SCSPFLPRTTPDNTTIEVEAENGGVKSHMTYRLLENIAKTEBPXIFRYVPGVIGIRM 152  |              |      | Q9PTB9 xenopus lae |
| QY                        | 121 IGIENIKPELAVSSDLKTYTTRFTVNSTSWMEVFAKXKDKXNTYNTLGIQPTTEYVI 180 |              |      | Q8K4B4 mus musculu |

Db 153 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNPANRKNQKQYNTLGLQPTFEYVI 212  
QY 181 ALRCAYESKFSWDSQEKMGTEEAR 208  
Db 213 ALRCAYESKFSWDSQEKMGTEEAR 240

RESULT 2  
Q8N117 PRELIMINARY; PRT; 732 AA.  
ID Q8N117  
AC Q8N117  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Gp130-like monocyte receptor.  
OS Homo sapiens (Human).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21986187; Pubmed=11877449;  
RA Chillard N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;  
RT "A Novel Type I Cytokine Receptor is Expressed on Monocytes, Signals  
RT Proliferation, and Activates STAT-3 and STAT-5."  
RL J. Biol. Chem. 277:16831-16836 (2002).  
DR EMBL; AF486620; AAM27958.1; -  
DR InterPro; IPR002996; CRA.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PF00041; FN3; 1.  
DR SMART; SM00060; FN3; 3.  
KW Receptor.  
SQ SEQUENCE 732 AA; 82953 MW; 30F84BD3D99A20E CRC64;

Query Match 100.0%; Score 1121; DB 4; Length 732;  
Best Local Similarity 100.0%; Pred. No. 8.7e-98;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 60  
Db 20 ALPAKPNISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 79  
QY 61 SCGFPLPRITIPDNYTTEVEAENGQVYKSHMTYRWLENIATKTEPPKIFRYKPVLGIR 120  
Db 80 SCGFPLPRITIPDNYTTEVEAENGQVYKSHMTYRWLENIATKTEPPKIFRYKPVLGIR 139  
QY 121 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNPANRKNQKQYNTLGLQPTFEYVI 180  
Db 140 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNPANRKNQKQYNTLGLQPTFEYVI 199  
QY 181 ALRCAYESKFSWDSQEKMGTEEAR 208  
Db 200 ALRCAYESKFSWDSQEKMGTEEAR 227

RESULT 3  
Q8K5B1 PRELIMINARY; PRT; 716 AA.  
ID Q8K5B1  
AC Q8K5B1  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Gp130-like monocyte receptor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21986187; Pubmed=11877449;  
RA Chillard N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;  
RT "A Novel Type I Cytokine Receptor is Expressed on Monocytes, Signals

RT Proliferation, and Activates STAT-3 and STAT-5."  
RL J. Biol. Chem. 277:16831-16836 (2002).  
DR EMBL; AF486621; AAM27959.1; -  
DR MGD; MGI:2180511; GIMR.  
DR InterPro; IPR002996; CRA.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PF00041; FN3; 1.  
DR SMART; SM00060; FN3; 3.  
KW Receptor.  
SQ SEQUENCE 716 AA; 80641 MW; 39E6B0B253F7C7E5 CRC64;

Query Match 44.8%; Score 502.5; DB 11; Length 716;  
Best Local Similarity 49.8%; Pred. No. 4.1e-39;  
Matches 104; Conservative 29; Mismatches 59; Indels 17; Gaps 5;

QY 2 LPKAPENISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 61  
Db 20 LPKAPENISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 71  
QY 62 SCGFPLPRITIPDNYTTEVEAENGQVYKSHMTYRWLENIATKTEPPKIFRYKPVLGIR 119  
Db 72 ASYSPFRSCAMPDICSVEVQKNGDGKYSITVYHLLISIAKTEPPIILSVNP1--CNR 129  
QY 120 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNPANRKNQKQYNTLGLQPTFEYVI 179  
Db 130 MFQIQW-KPERKTRGPFVCMRLFRVTNSRWTEVNF---ENCKQVCNLTGLQAFTEYV 184  
QY 180 IALRCAYESKFSWDSQEKMGTEEAR 208  
Db 185 LALRFPRNDRYMSKSKSEETRWTEEAR 213

RESULT 4  
Q8R501 PRELIMINARY; PRT; 716 AA.  
ID Q8R501  
AC Q8R501  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Cytokine receptor NR10.  
GN GIMR OR NR10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;  
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine  
RT receptor NR10."  
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AB083111; BAB86745.1; -  
DR MGD; MGI:2180511; GIMR.  
DR InterPro; IPR002996; CRA.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PF00041; FN3; 1.  
DR SMART; SM00060; FN3; 3.  
KW Receptor.  
SQ SEQUENCE 716 AA; 80598 MW; CBF718DCCD40FC7 CRC64;

Query Match 44.8%; Score 502.5; DB 11; Length 716;  
Best Local Similarity 49.8%; Pred. No. 4.1e-39;  
Matches 104; Conservative 29; Mismatches 59; Indels 17; Gaps 5;

QY 2 LPKAPENISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 61  
Db 20 LPKAPENISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 71  
QY 62 SCGFPLPRITIPDNYTTEVEAENGQVYKSHMTYRWLENIATKTEPPKIFRYKPVLGIR 119  
Db 72 ASYSPFRSCAMPDICSVEVQKNGDGKYSITVYHLLISIAKTEPPIILSVNP1--CNR 129

QY 120 MGIEMIKPELAPVSSDKYTLRFTVNSTSMVEVNFPAKRDKNQNTNLGLQPTTEVY 179  
DB 130 MFOIOM-KPREKTRGFPVLCMIRFRTVNSTSMVEVNF-----ENCKQVNCNLTLGLQPTTEVY 184  
QY 180 IALRCAYKESKFWSDMSQEKMGMTTEBEAP 208  
DB 185 LALRFRFNDSRYSKMSKEETVTLVEEVP 213

RESULT 5  
057519 PRELIMINARY; PRT; 881 AA.  
AC 057519,  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Gp130p1.  
GN XGp130.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen J., Grace A., Chien K.R.;  
RT "Partial characterization of putative Xenopus gp130."  
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF041845; AAC03531.1; -.  
DR HSSP; P40189; 1BQJ.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hemtopoptn\_L\_F2.  
DR Pfam; PF00041; fn3; 4.  
DR SMART; SMO0060; FN3; 3.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 25.6%; Score 287; DB 13; Length 881;  
Best Local Similarity 33.0%; Pred. No. 1.5e-18;  
Matches 69; Conservative 35; Mismatches 91; Indels 14; Gaps 6;

QY 3 PAKPENISCVYYRRKNLTCTWSPGKETS-YQYVRYA-FGEKNDCTNSTSENKA 60  
DB 122 PDKPTNLTCTIVYVNDLCTWDPGRPTNLPNTYLSHRAHFGAVYCRGANN----- 173  
QY 61 SCSEFLPRTTIPDNTTIEVAENGCVTASHMTYRLNIATPEPKIRYKPVLGISKM 120  
DB 174 SCTHSPGFQFYIDTTFQVEATNELGIQSEFLTTIDPVNIIVKPNPQISELSSILEPVA 233  
QY 121 IGIEWIKPELAPVSSDKYTLRFTVNSTSMVEVNFPAKRDKNQNTNLGLQPTTEVY 180  
DB 234 LKIEWKNP--TINAFLKTNINIRPVKTDW--EMVPEEDTASHRDSFTLQDLIPNTVEV 290  
QY 181 ALRCAYKESK-FWSDMSQEKMGMTTEBEAP 208  
DB 291 SIRCIKHQGHGFWSDMSSELKQVTPPEAP 319

RESULT 6  
09M6U9 PRELIMINARY; PRT; 918 AA.  
AC 09M6U9,  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Glycoprotein 130 precursor.  
GN Gp130.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryonic heart;  
RX MEDLINE=99026068; PubMed=9806927;  
RA Geislen M., Heller S., Pennica D., Ernberger U., Rohrer H.;  
RT "The specification of sympathetic neurotransmitter phenotype depends  
on gp130 cytokine receptor signaling."  
RL Development 125:4791-4801(1998).  
DR EMBL; AJ011688; CAB42084.1; -.  
DR HSSP; P40189; 1BQJ.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hemtopoptn\_L\_F2.  
DR Pfam; PF00041; fn3; 4.  
DR SMART; SMO0060; FN3; 4.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KW Signal.  
FT SIGNAL. 1 26 POTENTIAL.  
SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613BF CRC64;

Query Match 24.8%; Score 278; DB 13; Length 918;  
Best Local Similarity 27.7%; Pred. No. 1.1e-17;  
Matches 64; Conservative 47; Mismatches 66; Indels 54; Gaps 9;

QY 3 PAKPENISCVYYRRKNLTCTWSPGKETS-YQYVRYA-FGEKNDCTNSTSEN 58  
DB 129 PEKPNLSCTIVYLSPKVEWYNNCTNPPRHFTL-----DT 163  
QY 59 RASCSEFLPRTTIPDNTTIEVAENGCVTASHMTYRLNIATPEPKIRYKPVLGISKM 98  
DB 164 RFLRYKMPRETFPPDCIPEYVNSCTISDVQFVNLVFWVAANALGAESDHLVDFDIE 223  
QY 99 NIAKTEPKIRYKPVLGISKMIOIEWIKPELAPVSSDKYTLRFTVNSTSMVEVNFPAK 158  
DB 224 -IVKPPPPRNLSVNSGI-LPVLKLSW-ENOISTYMEKIRIRIRISSDTNMEVPP-DE 279  
QY 159 NRKDNQNTNLGLQPTTEVYIALRCAYKES-KFWSMSQEKMGMTTEBEAP 208  
DB 280 DTASPRTSFSGIQLRPYTEVYFSIRCKMEDGVGFWSDMSSEGIQVTTEDKP 330

RESULT 7  
09UHNS PRELIMINARY; PRT; 422 AA.  
AC 09UHNS,  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Class I cytokine receptor.  
GN ZCYTOR5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lok S., Presnell S.R., Jellberg A.C., Gilbert T., Whitmore T.E.,  
Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;  
RT Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF178684; AAD54385.1; -.  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SMO0060; FN3; 2.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Receptor.  
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 20.6%; Score 231; DB 4; Length 422;  
Best Local Similarity 29.2%; Pred. No. 1.2e-13;  
Matches 66; Conservative 34; Mismatches 90; Indels 36; Gaps 10;

QY 3 PAKPENISCVYYRRKNTCTWSPGK--ET-SYQYTVKRTYAFGEKNDCTNSSTSENR 59  
DB 135 PEKPNISCVSKMKMDLCTGWTGAGETFLHTNYSLKYLKRWYGQDNTCEBYHTVGP 193  
QY 60 ASC-----SFLPRITIPDNTYIEVEAENGDVISKSHMTYRLNIATKEPPKIRVXP 113  
DB 194 -SCHIRKDLALFTF-----YEIWEATNRLGSARSDVLTLDLVVTTDPPPEVHVS 245  
QY 114 VLGIKEMIQIEMIKELAPVSSDL---KYLRFRTVNSTSMWEVNFANRKKDKQNTY 169  
DB 246 VGLLEDQLSVRWVSP---PALKDPLFOAKYQIRYVEDSDMKVVDVSNQ-----TSCRL 298  
QY 170 TGLQPFTEYVIALRC-----AVKSKFWSMDSQEKMGT-BEAP 208  
DB 299 AGHKPGTYFVQVRCNPFYIGSKKAGIMSESHPTAASPRSERP 344  
RESULT 8  
ID 075462 PRELIMINARY; PRT; 422 AA.  
AC 075462;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Cytokine-like factor-1 precursor.  
GN CLF-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 11)  
RP SEQUENCE FROM N.A.  
RA Elson G.C.A., Graber P., Loebinger P., Herren S., Greener D.,  
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.,  
RT "CLF-1, a Novel Soluble Protein Shares Homology with Members of the  
RT Cytokine Type-1 Receptor Family.",  
RN J. Immunol. 0:0-0(1998).  
RL 12)  
RP SEQUENCE FROM N.A.  
RA Magrangeas F., Jacques Y., Minvielle S.,  
RT "Cloning and expression of a novel soluble protein containing  
RT hematopoietic cytokine receptor domain.",  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF059293; AAC28335.1; -  
DR EMBL; AF073515; AAC39681.1; -  
DR HSSP; P16471; 1BP3.  
DR Genew; HGNC:2364; CRLL1.  
DR InterPro; IPR002996; CRIL.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR007110; IG\_1like.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PSS0835; IG\_Like; 1.  
KM Receptor; Signal.  
FT SIGNAL 1 37  
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.  
SQ SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;  
Query Match 20.6%; Score 231; DB 4; Length 422;  
Best Local Similarity 29.2%; Pred. No. 1.2e-13;  
Matches 66; Conservative 34; Mismatches 90; Indels 36; Gaps 10;  
QY 3 PAKPENISCVYYRRKNTCTWSPGK--ET-SYQYTVKRTYAFGEKNDCTNSSTSENR 59  
DB 135 PEKPNISCVSKMKMDLCTGWTGAGETFLHTNYSLKYLKRWYGQDNTCEBYHTVGP 193  
QY 60 ASC-----SFLPRITIPDNTYIEVEAENGDVISKSHMTYRLNIATKEPPKIRVXP 113  
DB 194 -SCHIRKDLALFTF-----YEIWEATNRLGSARSDVLTLDLVVTTDPPPEVHVS 245  
QY 114 VLGIKEMIQIEMIKELAPVSSDL---KYLRFRTVNSTSMWEVNFANRKKDKQNTY 169

DB 246 VGLLEDQLSVRWVSP---PALKDPLFOAKYQIRYVEDSDMKVVDVSNQ-----TSCRL 298  
QY 170 TGLQPFTEYVIALRC-----AVKSKFWSMDSQEKMGT-BEAP 208  
DB 299 AGHKPGTYFVQVRCNPFYIGSKKAGIMSESHPTAASPRSERP 344  
RESULT 9  
ID 09JMS8 PRELIMINARY; PRT; 425 AA.  
AC 09JMS8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Cytokine receptor like molecule 3 precursor.  
GN CRLL1 OR CRLL3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN 11)  
RP SEQUENCE FROM N.A.  
RA Hirayama T., Iwama A., Nakamura Y., Nakauchi H.,  
RT "Cytokine receptor like molecule 3.",  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB040038; BAA92777.1; -  
DR HSSP; P16471; 1BP3.  
DR MGD; MG1:1340030; CRLL1.  
DR InterPro; IPR002996; CRIL.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
KM Receptor; Signal.  
FT SIGNAL 1 34  
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;  
Query Match 20.4%; Score 229; DB 11; Length 425;  
Best Local Similarity 29.2%; Pred. No. 1.9e-13;  
Matches 66; Conservative 34; Mismatches 90; Indels 36; Gaps 10;  
QY 3 PAKPENISCVYYRRKNTCTWSPGK--ET-SYQYTVKRTYAFGEKNDCTNSSTSENR 59  
DB 138 PEKPNISCVSKMKMDLCTGWTGAGETFLHTNYSLKYLKRWYGQDNTCEBYHTVGP 196  
QY 60 ASC-----SFLPRITIPDNTYIEVEAENGDVISKSHMTYRLNIATKEPPKIRVXP 113  
DB 197 -SCHIRKDLALFTF-----YEIWEATNRLGSARSDVLTLDLVVTTDPPPEVHVS 248  
QY 114 VLGIKEMIQIEMIKELAPVSSDL---KYLRFRTVNSTSMWEVNFANRKKDKQNTY 169  
DB 249 VGLLEDQLSVRWVSP---PALKDPLFOAKYQIRYVEDSDMKVVDVSNQ-----TSCRL 301  
QY 170 TGLQPFTEYVIALRC-----AVKSKFWSMDSQEKMGT-BEAP 208  
DB 302 AGHKPGTYFVQVRCNPFYIGSKKAGIMSESHPTAASPRSERP 347  
RESULT 10  
ID 09BEG2 PRELIMINARY; PRT; 861 AA.  
AC 09BEG2;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE IL-12 receptor beta2 precursor.  
GN IL-12R BETA2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OX NCBI\_TaxID=9913;  
RN 11)  
RP SEQUENCE FROM N.A.

RC TISSUE=Lymph node;  
 RA Waldvogel A.S., Zakher A., Heusler V.T.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ308426; CAC28320.1; -  
 DR HSSP; P40189; 180U.  
 DR InterPro; IPR002986; CRA.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hemloptn\_L\_F2.  
 DR Pfam; PFO0041; fn3; 3.  
 DR SMART; SMO0060; fn3; 4.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KM Receptor; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 861  
 SQ SEQUENCE 861 AA; 96208 MW; 4B7B1ESD1E358E5B CRC64;

Query Match 18.6%; Score 209; DB 6; Length 861;  
 Best Local Similarity 31.6%; Pred. No. 3.6e-11;  
 Matches 68; Conservative 28; Mismatches 95; Indels 24; Gaps 9;

QY 2 LPAKPNISCVYY-YRKNLTCTWSPKETS-YTQYTVKRYAFGEKHNDCTNSSTSE-- 57  
 DB 123 VEPQPNVNSCMQKGERGVTCVTHRGDRDHLTYATLQLN---GPK--NLTWQKCSQDY 177  
 QY 58 -NRASCFFLPRTIPDNTTIEVEANGDVKSHMTYRLNIAKTEPPKIFRYKPVUG 116  
 DB 178 CHLDLGINLTPESLESSYVKTALNSIGSASSFPFSLDLYVPLPMDIRIKFYNA 237  
 QY 117 IKRMIOIEMIKPELAVSSDKYTLFRVNSTSMWEVNF--AKNRKDKQYTNLTGLQPT 174  
 DB 238 SVDRCTLLWRDEGLV-----LNLRLKYPVRSNMVNVYNAKGHH-----LIDLKP 286  
 QY 175 FTEYVIALRCAYKSK-FWSDMSQEKMGTEEEAP 208  
 DB 287 FTEYERQISSKHLTKYKGSWSDMSSESLRTQPEEP 321

## RESULT 11

057520 PRELIMINARY; PRT; 710 AA.  
 ID 057520;  
 AC 057520;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE GPI30P3 (Fragment).  
 GN XGPI30.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCB1\_Taxid=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Chen J., Grace A., Chien K.R.;  
 RL "Partial characterization of putative Xenopus gpi30.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF041846; AAC03532.1; -  
 DR HSSP; P40189; 180U.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hemloptn\_L\_F2.  
 DR Pfam; PFO0041; fn3; 4.  
 DR SMART; SMO0060; fn3; 3.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 710 AA; 79849 MW; BFA7C77E32B6CE6F CRC64;

Query Match 18.2%; Score 204; DB 13; Length 710;  
 Best Local Similarity 30.9%; Pred. No. 8.6e-11;  
 Matches 47; Conservative 31; Mismatches 70; Indels 4; Gaps 3;  
 QY 58 NRASCFFLPRTIPDNTTIEVEANGDVKSHMTYRLNIAKTEPPKIFRYKPVUG 117

DB 1 NSGSCSIFPEPQFVDTTLQVEVKNELGQSDTLTVDPVNIKPNPEVSDLLISAVEL 60  
 QY 118 KMIOIEMIKPELAVSSDKYTLFRVNSTSMWEVNFARXKXKQYTNLTGLQFPE 177  
 DB 61 PNAKIKRMNPLNFT--LKTINIRYRYKQDM-EMVPEEDTASHRDSFTLQDLIPYE 117  
 QY 178 VYIALRCAYKSK-FWSDMSQEKMGTEEEAP 208  
 DB 118 YEVSIRKICEDGRGFWSDMSSEVKKQVTPBAQ 149

## RESULT 12

08WN24 PRELIMINARY; PRT; 848 AA.  
 ID 08WN24;  
 AC 08WN24;  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Interleukin-12 receptor beta 2 chain (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 OC NCB1\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Solano-Aguliar G.I., Zarlena D.S., Beshah E., Vengroski K.,  
 RA Gasparre L.C., Junker D., Cochran M., Weston C., Valencia D.,  
 RA Chiang C., Lunney J.K.;  
 RT "Limited effect of recombinant porcine interleukin-12 on porcine  
 lymphocytes due to a low expression of IL-12 beta2 receptor."  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF48143; AAL60218.1; -  
 DR InterPro; IPR002996; CRA.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hemloptn\_L\_F2.  
 DR Pfam; PFO0041; fn3; 4.  
 DR SMART; SMO0060; fn3; 4.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KM Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 848 848  
 SQ SEQUENCE 848 AA; 94753 MW; AD6C885A27DA427 CRC64;

Query Match 18.1%; Score 203; DB 6; Length 848;  
 Best Local Similarity 30.5%; Pred. No. 1.3e-10;  
 Matches 65; Conservative 31; Mismatches 97; Indels 20; Gaps 9;

QY 2 LPAKPNISCVYY-YRKNLTCTWSPKETS-YTQYTVKRYAFGEKHNDCTNSSTSE-- 57  
 DB 112 VEPQPNVNSCMQKGERGVTCVTHRGDRDHLTYATLQLN---GPK--NLTWQKCSQDY 166  
 QY 58 -NRASCFFLPRTIPDNTTIEVEANGDVKSHMTYRLNIAKTEPPKIFRYKPVUG 116  
 DB 167 CSDLGINLTPESLESSYVKTALNSIGSASSFPFSLDLYVPLPMDIRIKFYNA 226  
 QY 117 IKRMIOIEMIKPELAVSSDKYTLFRVNSTSMWEVNFARXKXKQYTNLTGLQFPT 176  
 DB 227 SMSSTGLQWRDGLV-----LNLRLKYPVRSNMVNVYNAKGHH-----HDLVLDKPT 277  
 QY 177 EYVIALRCAYKSK-FWSDMSQEKMGTEEEAP 208  
 DB 278 EYEFQISSKPHLQKRWSDMSSESLRTQPEEP 310

## RESULT 13

08MJS1 PRELIMINARY; PRT; 861 AA.  
 ID 08MJS1;  
 AC 08MJS1;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Interleukin-12 receptor beta 2.  
 OS Sus scrofa (Pig).

OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
FN [1]  
RP SEQUENCE FROM N.A.  
RA Kokubo T.;  
RT "Cloning of porcine interleukin-12 receptor beta 2 gene.";  
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF330213; AM447543.1; -  
DR InterPro: IPR002996; CR1A.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hemkopoptn\_L\_F2.  
DR Pfam: SM00041; fn3; 3.  
DR SMART: SM00060; FN3; 4.  
DR PROSITE: PS01353; HEMATOPO\_NEC\_L\_F2; 1.  
KW Receptor.  
SO SEQUENCE 861 AA; 96055 MW; 2AB63E3C5F4253A CRC64;

|                       |        |                  |        |                |
|-----------------------|--------|------------------|--------|----------------|
| Query Match           | 17.7%; | Score 198;       | DB 6;  | Length 861;    |
| Best Local Similarity | 30.0%; | Pred. No. 4e-10; |        |                |
| Matches               | 64;    | Conservative     | 32;    | Mismatches 97; |
|                       |        |                  | Indels | 20;            |
|                       |        |                  | Gaps   | 9;             |

```

Oy 2 LPAPENISCVY-YRNKLITCTSPKETS-TOYTVKRVAFGKHNCJTNSTSE-- 57
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 123 VPEBPQVNSCMQMGEGKGTACSMDBRDTHLYATLTLQLN--GPK-NLTWQCSDIY 177
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 58 -NRASCSFLLPRTITPDNYTIEVEAENGDVIKSHMTYWRLENIKTEPPKIFVKEVLG 116
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 178 CDSLDGDLNLPSPSPSSYTAQVTAIINSLGTASLSPTFTFLDVVRPLPPMDIRIKCVNA 237
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 117 IKRMITQTEMLKPELAVSSDLKTLTFRIVNSTSMWEVNPFAKORKQYTNLTGLOPFT 176
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 238 SVSTCTLTQMPDEGIV-----LNRKLRFRVYSRSMWVN-ATNAKGR---HDLVLDKPT 288
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 177 EYVALRCAYKESK-FMSDMSQCKMTEEEAP 208
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 289 EYEFQISKRHLQGRMSWSBSLRTQTEKGP 321
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

## RESULT 14

```

ID      08C7G1;                                PR1;      292 AA.
AC      08C7G1;
DT      01-MAR-2003 (TREMBLrel. 23, Created)
DT      01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Prolactin receptor related sequence 1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10099;
RN
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Liver;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RL      Nature 420:563-573(2002)".
DR      EMBL; AK050317; BAC34185.1; -.
SQ      SEQUENCE 292 AA; 33616 MW; 9D60422B5E88A19 CRC64;

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Query Match 17.3%; Score 194; DB 11; Length 292;  
Best Local Similarity 28.3%; Pred. No. 2.5e-10;  
Matches 58; Conservative 37; Mismatches 92; Indels 18; Gaps 10

[illegible]

```

Db      80 -SCFSSQKQTSIKIKIITIVNATNMGSGTSPFLVDVATYIVEEDEPPRNILLEKQYKDK 138
      118 KRMIOEMIKPELAPVSS---DLKTLSPRTYSMSMEVNFAPKRNKDKNQYULVLTGHP 174
      139 KYILMWKMLPPTITDVYKIGMFMTEIEIKLSBEDEW-EIHFTHGHP-----FVPPLYP 199
Qy      175 FTEYVIALRCAYVESKFFMSDMSQEK 199
      194 GKRLIVQTRCK-PDHGYMSRMQDEK 217
Db

```

RESULT 15

|    |  |              |           |                         |
|----|--|--------------|-----------|-------------------------|
| ID | Q99JZ1   | PRELIMINARY; | PRT;      | 608 AA.                 |
| AC | Q99JZ1   |              |           |                         |
| DT | 01-JUN-2001 (TREMBLrel. 17, Created)                               |              |           |                         |
| DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update)                  |              |           |                         |
| DT | 01-OCT-2002 (TREMBLrel. 22, Last annotation update)                |              |           |                         |
| DE | Prolactin receptor.  |              |           |                         |
| GN | PLRL.  |              |           |                         |
| OS | Mus musculus (Mouse).  |              |           |                         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |              |           |                         |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |              |           |                         |
| OX | NCBI_TaxID=10090;  |              |           |                         |
| RN | [1]  |              |           |                         |
| RP | SEQUENCE FROM N.A.   |              |           |                         |
| RA | Strausberg R.;   |              |           |                         |
| RL | Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.            |              |           |                         |
| DR | EMBL; BC005555; AAH0555.1; -.                                      |              |           |                         |
| DR | EMBL; BC006652; AAH06652.1; -.                                     |              |           |                         |
| DR | HSSP; P16471; 1BP3.  |              |           |                         |
| MD | MGI; MGI:97763; PrLr.  |              |           |                         |
| DR | InterPro; IPR002896; CRA1.   |              |           |                         |
| DR | InterPro; IPR003961; FN_III.                                       |              |           |                         |
| DR | InterPro; IPR003528; Hemtopoptn_L_F1.                              |              |           |                         |
| DR | Pfam; PF00041; FN3; 2.   |              |           |                         |
| DR | SMART; SMO0060; FN3; 2.  |              |           |                         |
| KR | PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.                            |              |           |                         |
| KM | Receptor.  |              |           |                         |
| SO | SEQUENCE   | 608 AA;      | 68223 MW; | 2710DAECGB1A8F63 CRC64; |

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 17.0%;           | Score 191;         | DB 11;     | Length 608; |
| Best Local Similarity | 27.8%;           | Pred. No. 1.2e-09; |            |             |
| Matches 57;           | Conservative 38; | Mismatches 92;     | Indels 18; | Gaps 10     |

```

QY 3 PAKPENISCVYYRRNLCTMSPGKETS-Y -TQYTKRITPA -EGEKND -NCTINSSYSEAR 59
   |||||:::|||||:::|||||:::|||||:::
Db 23 PGKPEIHKCRSPDKETFTCCMMNPGSDGGLPTNYSL -TYSKEGEKQYTYECPDYKTSGBP- 79
   |||||:::|||||:::|||||:::|||||:::
QY 60 ASCSEFLPRITIPDNYTIEVEAENDGVYKSHMTWRLENIAKTEPPK -IPRVKVLGI 117
   |||||:::|||||:::|||||:::|||||:::
Db 80 -SCFSPSKQYTSIMWKYIITVAATNMGSTSDPLVDYTYIYEPPEPRRLTLEVQKLKOK 138
   |||||:::|||||:::|||||:::|||||:::
QY 118 KRMIQIEMIKELAEVSS--DKYTLRFRTYNSTSMNEVNFAPAKRKDKQNYNLTLGLOP 174
   |||||:::|||||:::|||||:::|||||:::
Db 139 KTYLMTWKMLPTLITDVKTGMFTMEYEIRLKSEADEW- EIHFTGHQOTQ----FKVFDLYP 193
   |||||:::|||||:::|||||:::|||||:::
QY 175 FTEVYIALRCVAVKESKSPWSDMSQEK 199
   |||||:::|||||:::|||||:::
Db 194 GQKYLIVQTRCK -PDHGYVSRMGQER 217
   |||||:::|||||:::|||||:::

```

Search completed: August 18, 2003, 13:30:16  
Job time : 76.6152 secs

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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:12:37 ; Search time 71.829 Seconds  
(without alignments)  
417.649 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_544\_732

Perfect score: 1017  
Sequence: 1 KKPRLTTLCPWTPVNPAS.....VTAREFLVSEKLPHITNGEV 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 1017  | 100.0       | 620    | 22 | ABG05070    |
| 2          | 1017  | 100.0       | 732    | 23 | ABH05730    |
| 3          | 1017  | 100.0       | 764    | 24 | ABP54364    |
| 4          | 1017  | 100.0       | 764    | 24 | ABP54365    |
| 5          | 1010  | 99.3        | 745    | 23 | AAE24024    |
| 6          | 514.5 | 50.6        | 649    | 23 | ABH05738    |
| 7          | 514.5 | 50.6        | 662    | 22 | AAH51244    |
| 8          | 514.5 | 50.6        | 662    | 23 | AAE24029    |
| 9          | 514.5 | 50.6        | 662    | 23 | ABH05741    |

|    |       |      |      |    |          |
|----|-------|------|------|----|----------|
| 10 | 514.5 | 50.6 | 681  | 24 | ABP54363 |
| 11 | 505   | 49.7 | 94   | 24 | ABP54372 |
| 12 | 483.5 | 47.5 | 716  | 24 | ABP54370 |
| 13 | 483.5 | 47.5 | 726  | 23 | AAE24037 |
| 14 | 479.5 | 47.1 | 716  | 24 | ABP54371 |
| 15 | 462   | 45.4 | 652  | 22 | ABH51242 |
| 16 | 462   | 45.4 | 652  | 23 | AAE24028 |
| 17 | 304   | 29.9 | 662  | 23 | ABH05742 |
| 18 | 183   | 18.0 | 627  | 24 | ABP54366 |
| 19 | 96.5  | 9.5  | 851  | 19 | AAW43079 |
| 20 | 95.5  | 9.4  | 854  | 23 | ABH06214 |
| 21 | 95.5  | 9.4  | 854  | 24 | ABH06568 |
| 22 | 95    | 9.3  | 513  | 20 | AAW97587 |
| 23 | 95    | 9.3  | 849  | 21 | AAH69346 |
| 24 | 92    | 9.0  | 491  | 19 | AAW37057 |
| 25 | 92    | 9.0  | 858  | 23 | AAW48951 |
| 26 | 92    | 9.0  | 1294 | 23 | ABH78296 |
| 27 | 92    | 9.0  | 1349 | 19 | AAW59359 |
| 28 | 91.5  | 9.0  | 619  | 23 | AAU75156 |
| 29 | 91.5  | 9.0  | 646  | 23 | AAU75155 |
| 30 | 90.5  | 8.9  | 853  | 9  | AAH81858 |
| 31 | 90    | 8.8  | 486  | 19 | AAW37056 |
| 32 | 90    | 8.8  | 846  | 21 | AAH69353 |
| 33 | 89.5  | 8.8  | 853  | 22 | AAH82762 |
| 34 | 89    | 8.8  | 883  | 22 | AAH82761 |
| 35 | 89    | 8.8  | 1846 | 22 | ABH63163 |
| 36 | 88    | 8.7  | 854  | 19 | AAW43076 |
| 37 | 87.5  | 8.6  | 449  | 23 | ABH69364 |
| 38 | 87    | 8.6  | 615  | 23 | ABH91483 |
| 39 | 87    | 8.6  | 848  | 23 | AAU11872 |
| 40 | 87    | 8.6  | 865  | 21 | AAH69354 |
| 41 | 86    | 8.5  | 503  | 22 | AAH83355 |
| 42 | 86    | 8.5  | 801  | 12 | AAH11742 |
| 43 | 85    | 8.5  | 846  | 11 | AAH08406 |
| 44 | 85.5  | 8.4  | 1258 | 21 | AAH80120 |
| 45 | 85.5  | 8.4  | 1258 | 22 | AAH98987 |

#### ALIGNMENTS

RESULT 1  
ID ABG05070 standard; Protein; 620 AA.  
AC ABG05070;  
DT 13-FEB-2002 (first entry)  
DE Novel human diagnostic protein #5061.  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW Food supplement; medical imaging; diagnostic; genetic disorder.  
OS Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX Dmanac RT, Liu C, Tang YT;  
XX WPI, 2001-639362/73.  
XX N-PSDB; AAS69257.  
XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
XX Claim 20, SEQ ID No 35429; 103bp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging or sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations in  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 620 AA;  
SO  
Query Match 100.0%; Score 1017; DB 22; Length 620;  
Best Local Similarity 100.0%; Pred. No. 1.2e-93;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKPNKLTLCMPVNPAPASSIATWHDGDFKDKLNKESDVSNTEDRLIKCSTPSDYL 60  
DB 432 KKPNKLTLCMPVNPAPASSIATWHDGDFKDKLNKESDVSNTEDRLIKCSTPSDYL 491  
QY VIDKL VVNFNGVNLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELVSPPEI 120  
DB 492 VIDKL VVNFNGVNLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELVSPPEI 551  
QY 121 PPKSQYLRSRMPEGTREPAKEQLLFGSGSLVDPHLCBEGAPNPYLKNSVTAREFLVSEK 180  
DB 552 PPKSQYLRSRMPEGTREPAKEQLLFGSGSLVDPHLCBEGAPNPYLKNSVTAREFLVSEK 611  
QY 181 LPEHTKGEV 189  
DB 612 LPEHTKGEV 620  
RESULT 2  
ABBO5730  
ID ABB05730 standard; Protein; 732 AA.  
XX  
XX ABB05730;  
XX  
XX 01-MAY-2002 (first entry)  
XX  
XX Human zcytor17 protein sequence SEQ ID NO:2.  
XX  
XX zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
KW antiinflammatory; antiviral; antitubercular; antitubercular; cytoskeletal;  
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW inflammatory disease; pancreatitis; inflammatory bowel disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200200721-A2.  
XX  
XX 03-JAN-2002.  
PD

XX  
XX 26-JUN-2001; 2001WO-US20484.  
XX  
XX 26-JUN-2000; 2000US-214282P.  
XX  
XX 29-JUN-2000; 2000US-214955P.  
XX  
XX 08-FEB-2001; 2001US-267963P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Sprecher CA, Preenell SR, Gao Z, Whitmore TE, Kuiper JL;  
PI Maurer MF;  
XX  
XX WPI; 2002-090519/12.  
XX  
XX N-PSDB; ABA93767.  
XX  
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
PT splenic, blood or bone disorders -  
XX  
XX Claim 18; Page 166-168; 235bp; English.  
XX  
XX The present invention describes a cytokine receptor designated zcytor17.  
CC zcytor17 has immunomodulatory, antiviral, antitubercular, cytoskeletal,  
CC antitubercular, antitubercular and muscular activities. The zcytor17  
CC proteins are useful for treating and diagnosing lymphoid, immune,  
CC inflammatory, splenic, blood or bone disorders. Agonists or  
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
CC immunity and for stimulating lymphocyte proliferation, such as in the  
CC treatment of infections involving immunosuppression, including certain  
CC viral infections. They are also useful for inducing cytotoxicity and  
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to  
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 732 AA;  
SO  
Query Match 100.0%; Score 1017; DB 23; Length 732;  
Best Local Similarity 100.0%; Pred. No. 1.5e-93;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKPNKLTLCMPVNPAPASSIATWHDGDFKDKLNKESDVSNTEDRLIKCSTPSDYL 60  
DB 544 KKPNKLTLCMPVNPAPASSIATWHDGDFKDKLNKESDVSNTEDRLIKCSTPSDYL 603  
QY 61 VIDKL VVNFNGVNLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELVSPPEI 120  
DB 604 VIDKL VVNFNGVNLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELVSPPEI 663  
QY 121 PPKSQYLRSRMPEGTREPAKEQLLFGSGSLVDPHLCBEGAPNPYLKNSVTAREFLVSEK 180  
DB 664 PPKSQYLRSRMPEGTREPAKEQLLFGSGSLVDPHLCBEGAPNPYLKNSVTAREFLVSEK 723  
QY 181 LPEHTKGEV 189  
DB 724 LPEHTKGEV 732  
RESULT 3  
ABP54364  
ID ABP54364 standard; Protein; 764 AA.  
XX  
XX ABP54364;  
XX  
XX 20-JAN-2003 (first entry)  
XX  
XX Human NR10.4 splicing variant protein SEQ ID NO:4.  
XX  
XX NR10; splicing variant; haematopoietic receptor; immunomodulator;  
KW haematopoietic factor; immunological disease;  
KW

KW haematopoietic disease; haematopoietic cell regulation.  
XX  
OS Homo sapiens.  
XX WO200277230-A1.  
XX  
XX 03-OCT-2002.  
XX  
XX 22-MAR-2002; 2002WO-JP02769.  
XX  
XX 26-MAR-2001; 2001JP-0087298.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Maeda M, Yaguchi N, Hasegawa M;  
XX  
XX WPI: 2003-018925/01.  
XX N-PSDB; ABQ83364.  
XX  
XX NR10 splicing variants of hematopoietin receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX  
XX Claim 1; Fig 6; 250pp; Japanese.  
XX  
XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (1). (1) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors, and developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietin receptor genes participate  
CC in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.4  
CC protein from the present invention.  
XX  
XX Sequence 764 AA:  
SQ  
Query Match 100.0%; Score 1017; DB 24; Length 764;  
Best Local Similarity 100.0%; Pred. No. 1.6e-93;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKPNTLTHCWPVTVPAPASSIATWHDGDFKDKLNKESDSDSVNTEDRILKCPSPSDXL 60  
DB 576 KKPNTLTHCWPVTVPAPASSIATWHDGDFKDKLNKESDSDSVNTEDRILKCPSPSDXL 635  
QY 61 VIDKLNVNFGNVLQEIFTDEARTGOENNIGSEKNGVYTCPPRPDCLGKSFPELPVSPRI 120  
DB 636 VIDKLNVNFGNVLQEIFTDEARTGOENNIGSEKNGVYTCPPRPDCLGKSFPELPVSPRI 695  
QY 121 PPRKQYLRSRMPEGTRPEAKQQLFSGQSLVPDHLCEGAPNPYLKNSVTAREFLVSEK 180  
DB 696 PPRKQYLRSRMPEGTRPEAKQQLFSGQSLVPDHLCEGAPNPYLKNSVTAREFLVSEK 755  
QY 181 LPEHTKGEV 189  
DB 756 LPEHTKGEV 764

RESULT 4  
ABP54365  
ID ABP54365 standard; Protein; 764 AA.  
XX  
XX ABP54365;  
XX  
XX 20-JAN-2003 (first entry)  
XX  
XX Human NR10.4 splicing variant protein SEQ ID NO.6.  
XX  
XX NR10; splicing variant; haematopoietin receptor; immunomodulator;  
KW haemostatic; haematopoietic factor; immunological disease;  
KW haematopoietic disease; haematopoietic cell regulation.  
XX  
OS Homo sapiens.

XX  
XX WO200277230-A1.  
XX  
XX 03-OCT-2002.  
XX  
XX 22-MAR-2002; 2002WO-JP02769.  
XX  
XX 26-MAR-2001; 2001JP-0087298.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Maeda M, Yaguchi N, Hasegawa M;  
XX  
XX WPI: 2003-018925/01.  
XX N-PSDB; ABQ83365.  
XX  
XX NR10 splicing variants of hematopoietin receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX  
XX Claim 1; Fig 7-9; 250pp; Japanese.  
XX  
XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (1). (1) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors, and developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietin receptor genes participate  
CC in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.4  
CC protein from the present invention.  
XX  
XX Sequence 764 AA:  
SQ  
Query Match 100.0%; Score 1017; DB 24; Length 764;  
Best Local Similarity 100.0%; Pred. No. 1.6e-93;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKPNTLTHCWPVTVPAPASSIATWHDGDFKDKLNKESDSDSVNTEDRILKCPSPSDXL 60  
DB 576 KKPNTLTHCWPVTVPAPASSIATWHDGDFKDKLNKESDSDSVNTEDRILKCPSPSDXL 635  
QY 61 VIDKLNVNFGNVLQEIFTDEARTGOENNIGSEKNGVYTCPPRPDCLGKSFPELPVSPRI 120  
DB 636 VIDKLNVNFGNVLQEIFTDEARTGOENNIGSEKNGVYTCPPRPDCLGKSFPELPVSPRI 695  
QY 121 PPRKQYLRSRMPEGTRPEAKQQLFSGQSLVPDHLCEGAPNPYLKNSVTAREFLVSEK 180  
DB 696 PPRKQYLRSRMPEGTRPEAKQQLFSGQSLVPDHLCEGAPNPYLKNSVTAREFLVSEK 755  
QY 181 LPEHTKGEV 189  
DB 756 LPEHTKGEV 764

RESULT 5  
AAE24024  
ID AAE24024 standard; Protein; 745 AA.  
XX  
XX AAE24024;  
XX  
XX 23-SEP-2002 (first entry)  
XX  
XX Human haematopoietin receptor 1 (HPR1) protein.  
XX  
XX Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;  
KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
KW osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;  
KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;



RESULT 6  
ID ABB05738  
AC ABB05738 standard; Protein; 649 AA.  
XX  
XX  
DT 01-MAY-2002 (first entry)  
XX  
XX  
DE Human zcytor17 protein sequence SEQ ID NO:46.  
XX  
XX  
KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
KW antiinflammatory; antiviral; antirheumatic; antiautistic; cyostatic;  
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW inflammatory disease; pancreatitis; inflammatory bowel disease.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200200721-A2.  
XX  
XX  
PD 03-JAN-2002.  
XX  
XX  
PF 26-JUN-2001; 2001WO-US20484.  
XX  
XX  
PR 26-JUN-2000; 2000US-214282P.  
XX  
PR 29-JUN-2000; 2000US-214955P.  
XX  
PR 08-FEB-2001; 2001US-267963P.  
XX  
XX  
PA (ZYMO) ZYMOGENETICS INC.  
XX  
XX  
PI Sprecher CA, Prensell SR, Gao Z, Whitmore TE, Kuiper JL;  
XX  
PI Maurer MF;  
XX  
XX  
DR MPI; 2002-090519/12.  
XX  
XX  
DR N-PSDB; ABA93803.  
XX  
XX  
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
XX  
XX  
PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
XX  
XX  
PT splenic, blood or bone disorders -  
XX  
XX  
PS Claim 18; Page 195-197; 235pp; English.  
XX  
XX  
CC The present invention describes a cytokine receptor designated zcytor17.  
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,  
CC antirheumatic, antiautistic and muscular activities. The zcytor17  
CC proteins are useful for treating and diagnosing lymphoid, immune,  
CC inflammatory, splenic, blood or bone disorders. Agonists or  
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
CC immunity and for stimulating lymphocyte proliferation, such as in the  
CC treatment of infections involving immunosuppression, including certain  
CC viral infections. They are also useful for inducing cytotoxicity and  
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
CC exemplification of the present invention.  
XX  
XX  
SQ Sequence 649 AA;  
XX  
XX  
Query Match 50.6%; Score 514.5; DB 23; Length 649;  
Best Local Similarity 94.2%; Pred. No. 6.1e-43;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
XX  
XX  
QY 1 KKPENKLTLCWPTVPNPASSSIATWAGDDFKDKLNKESDVSNTEDRLIKPCSTPSDKL 60  
DB 544 KKPENKLTLCWPTVPNPASSSIATWAGDDFKDKLNKESDVSNTEDRLIKPCSTPSDKL 603  
QY 61 VIDKLVTNFGNVLQEIFTDARTGOENNLGGEKNG---YVTC 100  
DB 61 VIDKLVTNFGNVLQEIFTDARTGOENNLGGEKNG---YVTC 100

DB 604 VIDKLVTNFGNVLQEIFTDARTGOENNLGGEKNGTRILISCP 646  
XX  
XX  
RESULT 7  
ID AAB51244  
AC AAB51244 standard; Protein; 662 AA.  
XX  
XX  
XX  
AC AAB51244;  
XX  
XX  
DT 26-MAR-2001 (first entry)  
XX  
XX  
DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.  
XX  
XX  
KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;  
KW immunoregulation; haematopoietic cell regulation; transmembrane;  
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;  
KW metal allergy; pollen allergy.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
XX  
PN WO200075314-A1.  
XX  
XX  
PD 14-DEC-2000.  
XX  
XX  
PF 01-JUN-2000; 2000WO-JP03556.  
XX  
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PR 02-JUN-1999; 99JP-0155797.  
XX  
PR 30-JUL-1999; 99JP-0217797.  
XX  
XX  
PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.  
XX  
XX  
PI Maeda M, Yaguchi N;  
XX  
XX  
XX  
DR MPI; 2001-061720/07.  
XX  
XX  
DR N-PSDB; AAC92350.  
XX  
XX  
PT Hematopoietin receptor protein NR10 for screening potential ligands for  
XX  
XX  
PT treatment of immune and hematopoietic disorders such as autoimmune  
XX  
XX  
PT diseases and allergies -  
XX  
XX  
PS Claim 1; Fig 13-14; 127pp; Japanese.  
XX  
XX  
CC The present sequence represents a human haemopoietin receptor protein  
CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane  
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule  
CC which participates in immunoregulation and haematopoietic cell  
CC regulation in vivo, and is useful in searching for haematopoietic  
CC factors capable of binding to the receptor. NR10 can be used for the  
CC identification of substances for the treatment and prevention of immune  
CC and haematopoietic disorders including autoimmune diseases and allergies  
CC such as metal and pollen allergy.  
XX  
XX  
SQ Sequence 662 AA;  
XX  
XX  
Query Match 50.6%; Score 514.5; DB 22; Length 662;  
Best Local Similarity 94.2%; Pred. No. 6.2e-43;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
XX  
XX  
QY 1 KKPENKLTLCWPTVPNPASSSIATWAGDDFKDKLNKESDVSNTEDRLIKPCSTPSDKL 60  
DB 557 KKPENKLTLCWPTVPNPASSSIATWAGDDFKDKLNKESDVSNTEDRLIKPCSTPSDKL 616  
QY 61 VIDKLVTNFGNVLQEIFTDARTGOENNLGGEKNG---YVTC 100  
DB 617 VIDKLVTNFGNVLQEIFTDARTGOENNLGGEKNGTRILISCP 659  
XX  
XX  
RESULT 8  
ID AAE24029  
AC AAE24029 standard; Protein; 662 AA.  
XX  
XX  
XX  
AC AAE24029;  
XX  
XX

DT 23-SEP-2002 (first entry)  
XX  
DE Human HPRI variant protein #3.  
XX  
KW Human: haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;  
KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
KW osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;  
KW anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease;  
KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
KW ischaemic disease; variant.  
XX  
XX Homo sapiens.  
XX  
XX MO200229060-A2.  
XX  
XX 11-APR-2002.  
XX  
XX 05-OCT-2001; 2001WO-US31634.  
XX  
XX 06-OCT-2000; 2000US-238706P.  
XX 13-OCT-2000; 2000US-240476P.  
XX 20-FEB-2001; 2001US-270282P.  
XX  
XX (IMMW ) IMMUNEX CORP.  
XX  
XX Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;  
XX  
XX WPI; 2002-330172/36.  
XX  
XX Human and murine hemapoietin receptor polypeptides HPRI and HPR2,  
PT useful for treating cell proliferation, metabolic, and reproductive  
PT hormone related conditions -  
PT  
XX  
XX Disclosure; Page 112-115; 136pp; English.  
XX  
XX The present invention relates to human and murine haematopoietin receptor  
XX polypeptides HPRI and HPR2. Sequences of the invention are useful for  
XX treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
XX anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
XX resulting from a lack of bone-forming cells. They are also useful for  
XX treating cell proliferation conditions such as leukaemia and tumour  
XX metastasis, osteoporosis resulting from an excess of bone-resorbing  
XX cells. HPR sequences are also useful for treating medical conditions and  
XX diseases such as cell proliferation, metabolic and reproductive hormone  
XX related conditions. They are useful for treating various haematologic and  
XX oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
XX carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
XX cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
XX cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
XX sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
XX squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
XX of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
XX dysplastic syndromes (including refractory anaemia, refractory anaemia  
XX with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
XX penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
XX myeloid metaplasia, osteoclast disorders that lead to bone loss such  
XX as osteoporosis including post-menopausal osteoporosis, periodontitis  
XX resulting in tooth loosening or loss, prosthesis loosening after joint  
XX replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
XX Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
XX dementia including Creutzfeld-Jacob disease, demyelinating neuropathy,  
XX Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
XX myasthenia gravis), chronic neuronal degeneration, stroke including  
XX cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful  
XX for treating various other disorders such as osteoporosis, obesity,  
XX deficient mammary development and infertility. The present sequence  
XX is human HPRI variant protein.

SQ Sequence 662 AA;  
Query Match 50.6%; Score 514.5; DB 23; Length 662;  
Best Local Similarity 94.2%; Pred No. 6 2e-43;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
QY 1 KKPNTLTLCPVTENPAPSSIAIWHGDFDKDNLKSSDSVNTEDRIKCPSPDKL 60  
DB 557 KKPNTLTLCPVTENPAPSSIAIWHGDFDKDNLKSSDSVNTEDRIKCPSPDKL 616  
QY 61 VLDKLVNPGNVLQRIPTDEARTGQNNLGGKNG---YVTP 100  
DB 617 VLDKLVNPGNVLQRIPTDEARTGQNNLGGKNGTRILLSCP 659  
RESULT 9  
ABB05741  
ID ABB05741 standard; Protein; 662 AA.  
XX  
XX ABB05741;  
XX  
XX 01-MAY-2002 (first entry)  
XX  
XX Human zcytor17 protein sequence SEQ ID NO:54.  
XX  
XX zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
XX antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
XX infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
XX inflammatory disease; pancreatitis; inflammatory bowel disease.  
XX  
XX Homo sapiens.  
XX  
XX MO200200721-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 26-JUN-2001; 2001WO-US20484.  
XX  
XX 26-JUN-2000; 2000US-214282P.  
XX 29-JUN-2000; 2000US-214955P.  
XX 08-FEB-2001; 2001US-267963P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujiiper JL;  
XX Maurer MF;  
XX  
XX WPI; 2002-090519/12.  
XX N-PSDB; ABA93808.  
XX  
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
XX useful for treating and diagnosing lymphoid, immune, inflammatory,  
XX splenic, blood or bone disorders -  
XX  
XX Example 1; Page 204-206; 235pp; English.  
XX  
XX The present invention describes a cytokine receptor designated zcytor17.  
XX zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
XX antirheumatic, antiarthritic and muscular activities. The zcytor17  
XX proteins are useful for treating and diagnosing lymphoid, immune,  
XX inflammatory, splenic, blood or bone disorders. Agonists or  
XX anti-zcytor17 antibodies are useful in stimulating cell-mediated  
XX immunity and for stimulating lymphocyte proliferation, such as in the  
XX treatment of infections involving immunosuppression, including certain  
XX viral infections. They are also useful for inducing cytotoxicity and  
XX for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
XX for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
XX sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
XX pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
XX chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
XX ABA93843 and ABB05730 to ABB05745 represent sequences used in the

CC exemplification of the present invention.

XX Sequence 662 AA;

Query Match 50.6%; Score 514.5; DB 23; Length 662;  
Best Local Similarity 94.2%; Pred. No. 6.2e-43;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPENKLTLCWPTVPNPAESSIATWGGDFKDKLANKESDDSVNTEDRILKPCSTPSDKL 60  
DB 557 KKPENKLTLCWPTVPNPAESSIATWGGDFKDKLANKESDDSVNTEDRILKPCSTPSDKL 616

QY 61 VIDKLNVNFGNVLQEIFTDEARTGQNNLIGERKNG--YVTC 100  
DB 617 VIDKLNVNFGNVLQEIFTDEARTGQNNLIGERKNGTRILSSCP 659

RESULT 10  
ID ABP54363 standard; Protein; 681 AA.

AC ABP54363;  
XX 20-JAN-2003 (first entry)

DE Human NR10.3 splicing variant protein SEQ ID NO:2.

KW NR10, splicing variant; haematopoietic receptor; immunomodulator;  
KW haemostatic; haematopoietic factor; immunological disease;  
KW haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

PN WO200277230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

XX WPI; 2003-018925/01.

DR N-PSDB; ABQ83363.

XX NR10 splicing variants of hematopoietic receptor proteins and encoded

PT genes, applicable in searching hematopoietic factors and developing

XX remedies for immunological and hematopoietic diseases -

PS Example 2; Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors, and developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietic receptor genes participate  
CC in in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.3  
CC protein from the present invention.

XX Sequence 681 AA;

Query Match 50.6%; Score 514.5; DB 24; Length 681;  
Best Local Similarity 94.2%; Pred. No. 6.5e-43;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPENKLTLCWPTVPNPAESSIATWGGDFKDKLANKESDDSVNTEDRILKPCSTPSDKL 60  
DB 576 KKPENKLTLCWPTVPNPAESSIATWGGDFKDKLANKESDDSVNTEDRILKPCSTPSDKL 635

QY 61 VIDKLNVNFGNVLQEIFTDEARTGQNNLIGERKNG--YVTC 100  
DB 636 VIDKLNVNFGNVLQEIFTDEARTGQNNLIGERKNGTRILSSCP 678

RESULT 11  
ID ABP54372 standard; Protein; 94 AA.

AC ABP54372;

XX 20-JAN-2003 (first entry)

DE Human NR10.4 exon CP10-4 amino acid sequence SEQ ID NO:21.

KW NR10, splicing variant; haematopoietic receptor; immunomodulator;  
KW haemostatic; haematopoietic factor; immunological disease;  
KW haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

PN WO200277230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

XX WPI; 2003-018925/01.

DR N-PSDB; ABQ83373.

XX NR10 splicing variants of hematopoietic receptor proteins and encoded

PT genes, applicable in searching hematopoietic factors and developing

XX remedies for immunological and hematopoietic diseases -

PS disclosure; Page 238-239; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors, and developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietic receptor genes participate  
CC in in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.4 exon  
CC CP10.4 amino acid sequence from the present invention.

XX Sequence 94 AA;

Query Match 49.7%; Score 505; DB 24; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4.2e-43;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 YVTCPPRPDCPIGKSEBELVPSPEIPRKSQYLRSRMPEGTPEAKQQLFSGQSLVDPH 155  
DB 1 YVTCPPRPDCPIGKSEBELVPSPEIPRKSQYLRSRMPEGTPEAKQQLFSGQSLVDPH 60

QY 156 LCEBGAHPNYLKNSTYARFLVSEKLPEHTKGEV 189  
DB 61 LCEBGAHPNYLKNSTYARFLVSEKLPEHTKGEV 94

RESULT 12  
ID ABP54370 standard; Protein; 716 AA.

XX ABP54370;





```

XX 01-JUN-2000; 2000WO-JP03556.
PF
XX
PR 02-JUN-1999; 99JP-0155797.
PR 30-JUL-1999; 99JP-0217797.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Yaguchi N;
XX
DR WPI; 2001-061720/07.
DR N-PSDB; AAC92337.
XX
PT Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies -
XX
XX
PS Claim 1; Fig 3-5; 127pp; Japanese.
XX
CC The present sequence represents a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell
CC regulation in vivo, and is useful in searching for haematopoietic
CC factors capable of binding to the receptor. NR10 can be used for the
CC identification of substances for the treatment and prevention of immune
CC and haematopoietic disorders including autoimmune diseases and allergies
CC such as metal and pollen allergy.
XX
SQ Sequence 652 AA;

```

```

Query Match      45.4%; Score 462; DB 22; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKPNKLTHTLCWPTVPNPASSIATWGGDDPKDKLNLKESDSDSVNTEDRIILKPCSTPSDKL 60
   |||||||
DB 557 KKPNKLTHTLCWPTVPNPASSIATWGGDDPKDKLNLKESDSDSVNTEDRIILKPCSTPSDKL 616
   |||||||
QY 61 VIDKLVVNFGNVLQEIFTDEARTGOE 86
   |||||||
DB 617 VIDKLVVNFGNVLQEIFTDEARTGOE 642

```

Search completed: August 18, 2003, 13:27:01  
 Job time : 72.829 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 13:24:23 ; Search time 23.344 Seconds  
(without alignments)  
342.555 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_544\_732

Perfect score: 1017  
Sequence: 1 KKPNTLTLHLCWPTVPNPAES.....VTAREFLVSEKLPHETKGEV 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 92    | 9.0         | 491    | 3     | US-08-889-841B-10 |
| 2          | 92    | 9.0         | 491    | 4     | US-09-419-362-10  |
| 3          | 92    | 9.0         | 1349   | 3     | US-08-938-291A-6  |
| 4          | 92    | 9.0         | 1349   | 4     | US-09-589-619-6   |
| 5          | 90.5  | 8.9         | 508    | 3     | US-08-472-240A-16 |
| 6          | 90.5  | 8.9         | 853    | 4     | US-09-206-551-13  |
| 7          | 90.5  | 8.9         | 872    | 3     | US-07-556-483-12  |
| 8          | 90    | 8.8         | 486    | 3     | US-08-889-841B-8  |
| 9          | 90    | 8.8         | 486    | 4     | US-09-419-362-8   |
| 10         | 86.5  | 8.5         | 855    | 4     | US-09-206-551-11  |
| 11         | 86.5  | 8.5         | 423    | 4     | US-09-252-991A-12 |
| 12         | 86    | 8.5         | 855    | 3     | US-07-556-483-14  |
| 13         | 86    | 8.5         | 855    | 3     | US-08-472-240A-5  |
| 14         | 85    | 8.4         | 887    | 3     | US-08-889-841B-28 |
| 15         | 84.5  | 8.3         | 495    | 3     | US-09-419-362-28  |
| 16         | 84.5  | 8.3         | 665    | 2     | US-08-448-603A-32 |
| 17         | 84    | 8.3         | 665    | 4     | US-08-448-603A-32 |
| 18         | 84    | 8.3         | 665    | 3     | US-09-134-075-32  |
| 19         | 84    | 8.3         | 665    | 4     | US-09-134-075-32  |
| 20         | 82    | 8.1         | 855    | 1     | US-08-022-835-6   |
| 21         | 82    | 8.1         | 855    | 2     | US-08-388-809-6   |
| 22         | 82    | 8.1         | 855    | 2     | US-08-647-714-6   |
| 23         | 81.5  | 8.0         | 474    | 3     | US-08-889-841B-36 |
| 24         | 81.5  | 8.0         | 474    | 3     | US-08-889-841B-39 |
| 25         | 81.5  | 8.0         | 474    | 4     | US-09-419-362-36  |
| 26         | 81.5  | 8.0         | 474    | 4     | US-09-419-362-39  |
| 27         | 81    | 8.0         | 364    | 3     | US-09-085-305-6   |

|    |    |     |     |   |                   |                   |
|----|----|-----|-----|---|-------------------|-------------------|
| 28 | 81 | 8.0 | 479 | 2 | US-08-037-816A-20 | Sequence 20, Appl |
| 29 | 81 | 8.0 | 479 | 2 | US-08-037-816A-24 | Sequence 24, Appl |
| 30 | 81 | 8.0 | 479 | 2 | US-08-530-146-20  | Sequence 20, Appl |
| 31 | 81 | 8.0 | 479 | 2 | US-08-530-146-24  | Sequence 24, Appl |
| 32 | 81 | 8.0 | 495 | 3 | US-08-889-841B-25 | Sequence 25, Appl |
| 33 | 81 | 8.0 | 495 | 4 | US-09-419-362-25  | Sequence 25, Appl |
| 34 | 81 | 8.0 | 502 | 4 | US-08-037-816A-16 | Sequence 16, Appl |
| 35 | 81 | 8.0 | 507 | 2 | US-08-037-816A-16 | Sequence 16, Appl |
| 36 | 81 | 8.0 | 507 | 2 | US-08-037-816A-28 | Sequence 28, Appl |
| 37 | 81 | 8.0 | 507 | 2 | US-08-530-146-16  | Sequence 16, Appl |
| 38 | 81 | 8.0 | 507 | 2 | US-08-530-146-28  | Sequence 28, Appl |
| 39 | 80 | 7.9 | 484 | 2 | US-08-037-816A-22 | Sequence 22, Appl |
| 40 | 80 | 7.9 | 484 | 2 | US-08-530-146-22  | Sequence 22, Appl |
| 41 | 80 | 7.9 | 491 | 2 | US-08-037-816A-18 | Sequence 18, Appl |
| 42 | 80 | 7.9 | 491 | 2 | US-08-530-146-18  | Sequence 18, Appl |
| 43 | 80 | 7.9 | 516 | 4 | US-08-817-441-48  | Sequence 48, Appl |
| 44 | 80 | 7.9 | 520 | 2 | US-08-037-816A-14 | Sequence 14, Appl |
| 45 | 80 | 7.9 | 520 | 2 | US-08-037-816A-26 | Sequence 26, Appl |

## ALIGNMENTS

```
RESULT 1
US-08-889-841B-10
; Sequence 10, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Bertman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 491
; TYPE: PRP
; ORGANISM: HIV
US-08-889-841B-10

Query Match          9.0%; Score 92; DB 3; Length 491;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 49; Conservative 23; Mismatches 69; Indels 72; Gaps 8;

QY 7 TLICMPYVNPAPSSSI--ATMHGDDFKKLNKESDSDSVNTEDRLKPCSTPSDKLVTDK 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 30 THACVPPTDNPQEVVLENTENFNMMKNMVEQMHEDIISLDQSLKCV---KLTPLC 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 LVVNFQNVVQLFTDEARTGQENNIGKNGKVYVTPRPDPCL---GK----- 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 86 VTLNCTNLNANNNTNANNNTNNTYTLGEMGERKNCSFNTTSLRDKGKKEVALFYKLDV 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 -----SFEELPVSPRIP-----PRKSOY 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 146 QINDSTNVRLLISCVTSVITQACPKVSPFPIPHYCAPAGFALCKKDKKFNGTGCKN-- 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 LRS-RMPBGTREPAEKQLFSGQSLVPHLCEE 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 204 VRTVQCTHGRIRVSVSTOLLNGS-----LAEE 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
US-09-419-362-10
; Sequence 10, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Bertman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
```

PRIOR APPLICATION NUMBER: US 08/889,841  
PRIOR FILING DATE: 1997-07-08  
PRIOR APPLICATION NUMBER: US 60/676,737  
PRIOR FILING DATE: 1996-07-08  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PasteSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 491  
TYPE: PRT  
ORGANISM: HIV  
US-09-419-362-10

Query Match 9.0%; Score 92; DB 4; Length 491;  
Best Local Similarity 23.0%; Pred. No. 0.12;  
Matches 49; Conservative 23; Mismatches 69; Indels 72; Gaps 8;

QY 7 THLCWPLVPBPASSI--ATWGGDDPFKDLNKESDVSVTEDRIILKPGSTPDKLVIDK 64  
DB 30 THACVFPDPPEQVLENTENFNMMKNMVEQMHEITISLWDOSLPCV---KLTPLC 85  
QY 65 LVNPGVNLQEIFTEARTGOENNLGEGKNGVYTCFPRDPL---GK----- 109  
DB 86 VTLNCNLEMANNTENANNNTNNTLGMERGERKNCSEFNITSLRDKGKEXALFYGLDV 145  
QY 110 -----SPEELVPSPEIP-----PKSQY 127  
DB 146 QIDNSTNYRLISCVTSVITQACPKVSFEPIPIHYCAPAGFALIKCKDKKENGTPCKN-- 203  
QY 128 LRS-RMPEGTRPEAKQOLLESGGSLVDPDHCEE 159  
DB 204 VRTVQCTHGIRPVSTQLNLS-----LAEE 230

## RESULT 3

US-08-938-291A-6  
Sequence 6, Application US/08938291A  
Patent No. 611/673  
GENERAL INFORMATION:  
APPLICANT: Lev, Sima  
APPLICANT: Plowman, Gregory D.  
APPLICANT: Schlessinger, Joseph  
TITLE OF INVENTION: RDBG PROTEINS AND RELATED  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: PasteSeq  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,291A  
FILING DATE: September 26, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,337  
FILING DATE: October 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 228/172  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 955-0440  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-938-291A-6

Query Match 9.0%; Score 92; DB 3; Length 1349;  
Best Local Similarity 19.3%; Pred. No. 0.51;  
Matches 47; Conservative 28; Mismatches 77; Indels 92; Gaps 8;

QY 22 IATWGGDDPFKDLNKESDVSNT-----TEDRIILKPGSTPDKL 60  
DB 363 IRTKMSNDLMDKIEBPEPEDTQDGLYRQGAPEFRVASSVEQLNITIEDEVSQPLAAPSRT 422  
QY 61 VIDKLNVNFG-----NLQEIFTEARTGOENNLGEGKNGVYTCFPRP 103  
DB 423 HTLLVLHGGTLLDTGADDPSSKKGDANTIANVFPTVRVHYPSALGRLAIRLVPCP--P 480  
QY 104 DCP-----LGKSFEEPLVS--PEIPPKSQY-----LRSRMPEG 135  
DB 481 VCSDAFALVSNLSPYSHDEGLSSQDHIPLAALPLATSSFOYGEAVATVQRANLAVG 540  
QY 136 TRPEAKQQLFSGQ-----SLVDPDHCEEAGAPPYLNKSVTAREFLVSEKLPEHT 185  
DB 541 DFIKSGEGMTFNQVCLIGDCVGGILAFDALCYSNQ-----VSSGSSSR 586  
QY 186 KGEV 189  
DB 587 RGSV 590

## RESULT 4

US-09-589-619-6  
Sequence 6, Application US/09589619  
Patent No. 6576442  
GENERAL INFORMATION:  
APPLICANT: Lev, Sima  
APPLICANT: Plowman, Gregory D.  
APPLICANT: Schlessinger, Joseph  
TITLE OF INVENTION: RDBG PROTEINS AND RELATED  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: PasteSeq  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/589,619  
FILING DATE: 07-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,291  
FILING DATE: September 26, 1997  
APPLICATION NUMBER: 60/027,337  
FILING DATE: October 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 228/172  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6662  
TELEFAX: (703) 836-2021

Db 178 IVPINDNSTNSTNYRI,INCNTSAITQACP-KVSEFPDPIH-YCAPAGFATLKCNDKREN 235

QY 132 -----MPEGRPEAKQQLFSGSLVDPHLCCE 159  
Db 236 GTGECTNVSTVQCTHGIRPVVSTQLLNGS-----LAEE 269

RESULT 7  
US-07-956-483-12  
Sequence 12, Application US/07956483  
Patent No. 6261799  
GENERAL INFORMATION:  
APPLICANT: KIENY, Marie-Paule  
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956,483  
FILING DATE: 31-DEC-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 92/19742  
FILING DATE: 12-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 05392  
FILING DATE: 02-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Crane-Feuzy, Sharon E  
REGISTRATION NUMBER: 36,113  
REFERENCE/DOCKET NUMBER: 017753-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 872 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-956-483-12

Query Match 8.8%; Score 90.5; DB 3; Length 872;  
Best Local Similarity 22.3%; Pred. No. 0.4;  
Matches 49; Conservative 21; Mismatches 63; Indels 87; Gaps 10;  
QY 7 THLCMPVTPNPAESSI--ATWHDGDFKDKLNKESDVSNTEDRIILKPCSTPSDKLVYDK 64  
Db 70 THACVPTDNPQEVVLENTENFNMKNMVEQMHEDIISLWDQSLKPCV-----KLTPLC 123  
QY 65 LVVNGNVQLIETDEARTG--OENNIGKRGVYTCPE-----RPD 104  
Db 124 LCVTLN-----CSDELRRNGTGMNVTTEKGMKNSFVVTIVLKDKQVYALFYRLD 177  
QY 105 -----CPGSGFEELPVSPETIPPKSGYLRSR----- 131  
Db 178 IVBIDDSSTNSNYRLINCNTSAITQACP-KVSFEPIPIH-YCAPGFAILKCRDKKN 235  
QY 132 -----MPEGRPEAKQQLFSGSLVDPHLCCE 159  
Db 236 GTGECTNVSTVQCTHGIRPVVSTQLLNGS-----LAEE 269

RESULT 8  
US-08-889-841B-8  
Sequence 8, Application US/0889841B  
GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
FILE REFERENCE: 14918-703CIP  
CURRENT APPLICATION NUMBER: US/08/889,841B  
CURRENT FILING DATE: 1997-07-08  
PRIOR APPLICATION NUMBER: US 60/676,737  
PRIOR FILING DATE: 1996-07-08  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 486  
TYPE: PRT  
ORGANISM: HIV  
US-08-889-841B-8

Query Match 8.8%; Score 90; DB 3; Length 486;  
Best Local Similarity 22.2%; Pred. No. 0.2;  
Matches 47; Conservative 20; Mismatches 75; Indels 70; Gaps 7;  
QY 7 THLCMPVTPNPAESSI--ATWHDGDFKDKLNKESDVSNTEDRIILKPCSTPSDKLVYDK 64  
Db 30 THACVPTDNPQEVVLENTENFNMKNMVEQMHEDIISLWDQSLKPCV-----KLTPLC 85  
QY 65 LVVNGNVQLIETDEARTGQENNIGKRGVYTCPE----- 102  
Db 86 VTILNCTNLENNANTNNTNNTYTLGEMERGEIKNSFNITSLRDKVKEVALFYKLDV 145  
QY 103 -----PDCPLKGSFEELPVSPETIPR-----KSGYLRSMP----- 133  
Db 146 QIDNSTNYRLISCVTSVITQACP-KVSFEPIPIH-YCAPGFAILKCRDKKFGTGPCKNV 204  
QY 134 -----EGTRPEAKQQLFSGSLVDPHLCCE 159  
Db 205 STVQCTHGIRPVVSTQLLNGS-----LAEE 230

RESULT 9  
US-09-419-362-8  
Sequence 8, Application US/09419362  
Patent No. 6585979  
GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
FILE REFERENCE: 14918-703DIPV  
CURRENT APPLICATION NUMBER: US/09/419,362  
CURRENT FILING DATE: 1999-10-15  
PRIOR APPLICATION NUMBER: US 08/889,841  
PRIOR FILING DATE: 1997-07-08  
PRIOR APPLICATION NUMBER: US 60/676,737  
PRIOR FILING DATE: 1996-07-08  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 486  
TYPE: PRT  
ORGANISM: HIV  
US-09-419-362-8

Query Match 8.8%; Score 90; DB 4; Length 486;  
Best Local Similarity 22.2%; Pred. No. 0.2;  
Matches 47; Conservative 20; Mismatches 75; Indels 70; Gaps 7;  
QY 7 THLCMPVTPNPAESSI--ATWHDGDFKDKLNKESDVSNTEDRIILKPCSTPSDKLVYDK 64  
Db 30 THACVPTDNPQEVVLENTENFNMKNMVEQMHEDIISLWDQSLKPCV-----KLTPLC 85  
QY 65 LVVNGNVQLIETDEARTGQENNIGKRGVYTCPE----- 102  
Db 86 VTILNCTNLENNANTNNTNNTYTLGEMERGEIKNSFNITSLRDKVKEVALFYKLDV 145

QY 103 -----PDCPLGKSFELPVSPPIPR-----KSOYLRSMP----- 133  
DB 146 QIDNSTNYRLISCTSVITQACP-KVSPFLIPHIHYCAPAGAILKCKDKKFNGTGPKCNV 204  
QY 134 -----EGTRPEAKEQLLFSGOSLVDPDHCE 159  
DB 205 STVQCTHGIRPVSTQLLNGS-----LAEE 230

## RESULT 10

US-09-206-551-11  
Sequence 11, Application US/09206551B  
Patent No. 6521739  
GENERAL INFORMATION:  
APPLICANT: Hahn, Beatrice H.  
APPLICANT: Gao, Feng  
APPLICANT: Marx, Preston A.  
APPLICANT: Shaw, George M.  
APPLICANT: Smith, Stephen M.  
APPLICANT: Georges-Courbot, Marie Claude  
APPLICANT: Lu, Chang Yong  
TITLE OF INVENTION: Complete Genome Sequences of a Simian  
TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
FILE REFERENCE: D6286  
CURRENT APPLICATION NUMBER: US/09/206,551B  
CURRENT FILING DATE: 1998-12-07  
NUMBER OF SEQ ID NOS: 58  
SEQ ID NO 11  
LENGTH: 855  
TYPE: PRV  
ORGANISM: Simian immunodeficiency virus  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of homologous region of  
US-09-206-551-11

Query Match 8.5%; Score 86.5; DB 4; Length 855;  
Best Local Similarity 24.0%; Pred. No. 1.1;  
Matches 47; Conservative 22; Mismatches 70; Indels 57; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWGGDDPKDLNLESDDSVNTEDRILKPC--STP--SDKLV 61  
DB 69 THACVPTDNPGEIDLVNVTSEFNWKNMVDQMEDIISLMDQSLKPCVKLTPLCVTL 128  
QY 62 IDKLNVNFGVNLQEIFTEBARTQEN-----NLGKXGVTTCPPRPD----- 104  
DB 129 CHNITINNTNNNTNI--TDGVREEMKNCSEFMTTELRDKQKXVSLFYRDIQINKTDNN 187  
QY 105 -----CPLGKSFELPVSPPIPRKSOYLRSMP----- 134  
DB 188 SYRLINCNTSTTQACP-KVSPFLIPHI-YCAPAGAILKCKDKKFNGTGPKCNVSTVOC 245  
QY 135 --GTRPEAKEQLLFSG 148  
DB 246 THGIRPVSTQLLNG 261

RESULT 11  
US-09-206-551-12  
Sequence 12, Application US/09206551B  
Patent No. 6521739  
GENERAL INFORMATION:  
APPLICANT: Hahn, Beatrice H.  
APPLICANT: Gao, Feng  
APPLICANT: Marx, Preston A.  
APPLICANT: Shaw, George M.  
APPLICANT: Smith, Stephen M.  
APPLICANT: Georges-Courbot, Marie Claude  
APPLICANT: Lu, Chang Yong  
TITLE OF INVENTION: Complete Genome Sequences of a Simian  
TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped

TITLE OF INVENTION: Mangabey  
FILE REFERENCE: D6286  
CURRENT APPLICATION NUMBER: US/09/206,551B  
CURRENT FILING DATE: 1998-12-07  
NUMBER OF SEQ ID NOS: 58  
SEQ ID NO 12  
LENGTH: 855  
TYPE: PRV  
ORGANISM: Simian immunodeficiency virus  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of homologous region of  
US-09-206-551-12

Query Match 8.5%; Score 86.5; DB 4; Length 855;  
Best Local Similarity 24.0%; Pred. No. 1.1;  
Matches 47; Conservative 22; Mismatches 70; Indels 57; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWGGDDPKDLNLESDDSVNTEDRILKPC--STP--SDKLV 61  
DB 69 THACVPTDNPGEIDLVNVTSEFNWKNMVDQMEDIISLMDQSLKPCVKLTPLCVTL 128  
QY 62 IDKLNVNFGVNLQEIFTEBARTQEN-----NLGKXGVTTCPPRPD----- 104  
DB 129 CHNITINNTNNNTNI--TDGVREEMKNCSEFMTTELRDKQKXVSLFYRDIQINKTDNN 187  
QY 105 -----CPLGKSFELPVSPPIPRKSOYLRSMP----- 134  
DB 188 SYRLINCNTSTTQACP-KVSPFLIPHI-YCAPAGAILKCKDKKFNGTGPKCNVSTVOC 245  
QY 135 --GTRPEAKEQLLFSG 148  
DB 246 THGIRPVSTQLLNG 261

## RESULT 12

US-09-252-991A-26008  
Sequence 26008, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 26008  
LENGTH: 423  
TYPE: PRV  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26008

Query Match 8.5%; Score 86; DB 4; Length 423;  
Best Local Similarity 31.9%; Pred. No. 0.44;  
Matches 30; Conservative 15; Mismatches 33; Indels 16; Gaps 5;

QY 12 PVPV-NPAESSIATWGGDDPKDLNLESDDSVNTEDRILKPCSTPDKLVTDKLVNFG 70  
DB 22 PTFPESVADGTVAITH-----KRGKAVKDELIV--DIETDKVILEVLAEDG 68  
QY 71 NVLQEIFTEBARTQENNLGKXGVTTCPPRP 103  
DB 69 -VLAELIKKNGDVTLSNELGLNKGAAAPAP 101

## RESULT 13

US-07-956-483-14  
Sequence 14, Application US/07956483

```
/ Patent No. 6261799
/ GENERAL INFORMATION:
/ APPLICANT: KIENY, Marie-Paule
/ TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/956,483
/ FILING DATE: 31-DEC-1992
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO 92/19742
/ FILING DATE: 12-NOV-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 91 05392
/ FILING DATE: 02-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Crane-Feury, Sharon E
/ REGISTRATION NUMBER: 36,113
/ REFERENCE/DOCKET NUMBER: 017753-005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 855 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-07-956-483-14

Query Match      8.5%; Score 86; DB 3; Length 855;
Best Local Similarity 29.6%; Pred. No. 1.2;
Matches 29; Conservative 19; Mismatches 42; Indels 8; Gaps 4;

QY 7 THLCWPTVNPASSI--ATWGGDDFKDKLNKESDVSNTEDRIKPCSTPSDKLVIDK 64
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 THACVPTDPNPQEVVIGNTVFNNMKNMNVGEQMHEDIISLWDQSLKPCV----KLTPLC 125
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 LVVNFQNVLOEFTDEARFGQENNLGGEKNGVYT-CPF 101
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 VTLNCTNLNDRSTNATNT-TSSNRKGMEGEMTNCSE 162
    : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-08-472-240A-5
/ Sequence 5, Application US/08472240A
/ Patent No. 6284248
/ GENERAL INFORMATION:
/ APPLICANT: KIENY, Marie-Paule
/ TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
```

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/472,240A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/956,483
/ FILING DATE: 31-DEC-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Teskin, Robin L.
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 017753-055
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 887 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..854
/ US-08-472-240A-5

Query Match      8.4%; Score 85; DB 3; Length 887;
Best Local Similarity 28.3%; Pred. No. 1.7;
Matches 28; Conservative 17; Mismatches 46; Indels 8; Gaps 3;

QY 7 THLCWPTVNPASSI--ATWGGDDFKDKLNKESDVSNTEDRIKPCSTPSDKLVIDK 64
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 THACVPTDPNPQEVVIGNTVFNNMKNMNVGEQMHEDIISLWDQSLKPCV----KLTPLC 129
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 LVVNFQNVLOEFTDEARFGQENNLGGEKNG--YVTCPE 101
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 VTLNCTNLNDRSTNATNTTSSNRKGKXEGEMTNCSE 168
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 15
US-08-889-841B-28
/ Sequence 28, Application US/08889841B
/ GENERAL INFORMATION:
/ APPLICANT: Bertman, Phillip W.
/ TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
/ FILE REFERENCE: 14918-703CIP
/ CURRENT APPLICATION NUMBER: US/08/889,841B
/ CURRENT FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: US 60/676,737
/ PRIOR FILING DATE: 1996-07-08
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: Faastsq for Windows Version 3.0
/ SEQ ID NO 28
/ LENGTH: 495
/ TYPE: PRT
/ ORGANISM: HIV
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1)...(495)
/ OTHER INFORMATION: Xaa = Any Amino Acid
/ US-08-889-841B-28

Query Match      8.3%; Score 84.5; DB 3; Length 495;
Best Local Similarity 20.7%; Pred. No. 0.82;
Matches 48; Conservative 20; Mismatches 67; Indels 97; Gaps 10;

QY 7 THLCWPTVNPASSIATWGGDDF--KDKLNKESDVSNTEDRIKPCSTPSDKLVIDK 64
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

Db      31  THACVPTDNNPCEIELVNV- VTEDFNMMKKKKMVDQGHEDIIILMDSELKPCVLTPLCLVLT  89
QY      54  -----STPBDKLVIDKLNVNFGVNLQEIPTDEARTQENNLGCKKNGYVTCPPR--- 102
           :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      90  NCSDVNNSTNPND-----TNTNSTNTTSTGPTATSTSEKK--EKGIKKCSFNIT  139
QY      103 -----PDCPLGKSFEBELPVSPELP-- 121
           :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      140 HMKDKVQKEYALFYKLDIVPIDDNNSTYRLISCNSTSVITQACPM-VTFEPIPIHYCAPAG  198
QY      122 -----PRK-----SOYLRSRMEEGTRPEAKEQILFSGQSLVDPHLCEE  159
           :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      139 FALIKCKDKKFFNGTGPCSKVSTYVQCHTHGRIPVSVTDLNLGSG-----LAEE  244

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:27:13 ; Search time 24.6912 Seconds  
(without alignments)  
1002.770 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_544\_732

Perfect score: 1017  
Sequence: 1 KKPNTLTLCHWPTVNPAS...VTAREFLVSEKLPHRTKGEV 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Published\_Applications\_AA.\*  
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3: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2          | 1010  | 99.3        | 745    | 11    | US-09-972-708-4   |
| 3          | 514.5 | 50.6        | 649    | 11    | US-09-892-949-46  |
| 4          | 514.5 | 50.6        | 662    | 11    | US-09-972-708-15  |
| 5          | 514.5 | 50.6        | 662    | 11    | US-09-892-949-54  |
| 6          | 514.5 | 50.6        | 662    | 15    | US-10-006-265-17  |
| 7          | 483.5 | 47.5        | 726    | 11    | US-09-972-708-12  |
| 8          | 462   | 45.4        | 652    | 11    | US-09-972-708-14  |
| 9          | 462   | 45.4        | 652    | 15    | US-10-006-265-2   |
| 10         | 304   | 29.9        | 854    | 12    | US-09-892-949-57  |
| 11         | 95.5  | 9.4         | 854    | 12    | US-10-190-435-5   |
| 12         | 95.5  | 9.4         | 854    | 12    | US-10-190-435-128 |
| 13         | 91.5  | 9.0         | 619    | 10    | US-09-891-609-4   |
| 14         | 91.5  | 9.0         | 646    | 10    | US-09-891-609-2   |
| 15         | 88.5  | 8.7         | 865    | 12    | US-10-190-435-140 |

|    |      |     |      |    |                     |                   |
|----|------|-----|------|----|---------------------|-------------------|
| 16 | 86.5 | 8.5 | 803  | 12 | US-10-190-435-134   | Sequence 134, App |
| 17 | 86.5 | 8.5 | 803  | 12 | US-10-190-435-135   | Sequence 135, App |
| 18 | 86   | 8.5 | 503  | 9  | US-09-759-841-4     | Sequence 4, Appl  |
| 19 | 85.5 | 8.4 | 1258 | 10 | US-09-922-543-1     | Sequence 1, Appl  |
| 20 | 84.5 | 8.3 | 858  | 12 | US-10-190-435-150   | Sequence 150, App |
| 21 | 83.5 | 8.2 | 853  | 12 | US-10-286-332A-33   | Sequence 33, Appl |
| 22 | 83.5 | 8.2 | 853  | 14 | US-10-003-035-33    | Sequence 33, Appl |
| 23 | 83.5 | 8.2 | 903  | 11 | US-09-746-783-142   | Sequence 142, App |
| 24 | 83.5 | 8.2 | 1101 | 12 | US-10-286-332A-53   | Sequence 53, Appl |
| 25 | 83.5 | 8.2 | 1101 | 14 | US-10-003-035-53    | Sequence 53, Appl |
| 26 | 83.5 | 8.2 | 1186 | 12 | US-10-286-332A-55   | Sequence 55, Appl |
| 27 | 83.5 | 8.2 | 1186 | 14 | US-10-003-035-55    | Sequence 55, Appl |
| 28 | 83   | 8.2 | 511  | 9  | US-09-864-761-34590 | Sequence 34590, A |
| 29 | 82.5 | 8.1 | 579  | 15 | US-10-032-162-15    | Sequence 15, Appl |
| 30 | 82.5 | 8.1 | 790  | 9  | US-09-765-519-2     | Sequence 2, Appl  |
| 31 | 82.5 | 8.1 | 849  | 15 | US-10-235-994-2     | Sequence 2, Appl  |
| 32 | 82.5 | 8.1 | 799  | 12 | US-10-190-435-148   | Sequence 148, App |
| 33 | 82.5 | 8.1 | 862  | 12 | US-10-190-435-141   | Sequence 141, App |
| 34 | 82.5 | 8.1 | 869  | 12 | US-10-190-435-4     | Sequence 4, Appl  |
| 35 | 82.5 | 8.1 | 870  | 12 | US-10-190-435-127   | Sequence 127, App |
| 36 | 82   | 8.1 | 506  | 10 | US-09-934-060A-24   | Sequence 24, Appl |
| 37 | 82   | 8.1 | 506  | 10 | US-09-934-060A-30   | Sequence 30, Appl |
| 38 | 82   | 8.1 | 556  | 10 | US-09-934-060A-6    | Sequence 6, Appl  |
| 39 | 82   | 8.1 | 720  | 10 | US-09-934-060A-2    | Sequence 2, Appl  |
| 40 | 82   | 8.1 | 720  | 10 | US-09-934-060A-4    | Sequence 4, Appl  |
| 41 | 82   | 8.1 | 1080 | 9  | US-09-904-380-2     | Sequence 2, Appl  |
| 42 | 81   | 8.0 | 100  | 15 | US-10-032-162-2     | Sequence 2, Appl  |
| 43 | 81   | 8.0 | 502  | 9  | US-09-796-202-16    | Sequence 16, Appl |
| 44 | 81   | 8.0 | 502  | 12 | US-10-323-314-16    | Sequence 16, Appl |
| 45 | 81   | 8.0 | 625  | 15 | US-10-032-162-17    | Sequence 17, Appl |

#### ALIGNMENTS

RESULT 1  
US-09-892-949-2  
; Sequence 2, Application US/09892949  
; Publication No. US20030096339A1  
GENERAL INFORMATION:  
; APPLICANT: Sprenger, Cindy A.  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Kuiper, Joseph L.  
; APPLICANT: Maurer, Mark F.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
; FILE REFERENCE: 00-42  
; CURRENT APPLICATION NUMBER: US/09/892,949  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,282  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,955  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/267,963  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: faustseq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 732  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-892-949-2  
Query Match 100.0%; Score 1017; DB 11; Length 732;  
Best Local Similarity 100.0%; Pred. No. 4.8e-97;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKPNTLTLCHWPTVNPASSTATWGDGDFDKLTKSSDSVYNEEDILKPCSPDKL 60  
DB 544 KKPNTLTLCHWPTVNPASSTATWGDGDFDKLTKSSDSVYNEEDILKPCSPDKL 603  
QY 61 VIDKLIVNFGVNLQRIFTDEARTGQENNLGGEKNGYVTCPPRPDCPLKSPFEELVSPDEI 120

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Db 604 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 663
QY 121 PPKSQYLRSRMPEGTRPEAKEQLLFSGOSLVDPDHLCEBGAPNPYLKNSVTAREFLVSEK 180
Db 664 PPKSQYLRSRMPEGTRPEAKEQLLFSGOSLVDPDHLCEBGAPNPYLKNSVTAREFLVSEK 723
QY 181 LPEHTKGEV 189
Db 724 LPEHTKGEV 732
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## RESULT 2

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US-09-972-708-4
; Sequence 4, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-4
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Query Match 99.3%; Score 1010; DB 11; Length 745;
Best Local Similarity 99.5%; Pred. No. 2.6e-96;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KKPKNLTLHCWPTVNPAPASSIATWGGDPFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
Db 557 KKPKNLTLHCWPTVNPAPASSIATWGGDPFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 120
Db 617 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 676
QY 121 PPKSQYLRSRMPEGTRPEAKEQLLFSGOSLVDPDHLCEBGAPNPYLKNSVTAREFLVSEK 180
Db 677 PPKSQYLRSRMPEGTRPEAKEQLLFSGOSLVDPDHLCEBGAPNPYLKNSVTAREFLVSEK 736
QY 181 LPEHTKGEV 189
Db 737 LPEHTKGEV 745
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## RESULT 3

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US-09-892-949-46
; Sequence 46, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prensell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuipert, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
```

```
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-46
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Query Match 50.6%; Score 514.5; DB 11; Length 649;
Best Local Similarity 94.2%; Pred. No. 8.3e-45;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
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QY 1 KKPKNLTLHCWPTVNPAPASSIATWGGDPFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
Db 544 KKPKNLTLHCWPTVNPAPASSIATWGGDPFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 603
QY 61 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 100
Db 604 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 646
```

## RESULT 4

```
US-09-972-708-15
; Sequence 15, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-15
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Query Match 50.6%; Score 514.5; DB 11; Length 662;
Best Local Similarity 94.2%; Pred. No. 8.5e-45;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
```

```
QY 1 KKPKNLTLHCWPTVNPAPASSIATWGGDPFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
Db 557 KKPKNLTLHCWPTVNPAPASSIATWGGDPFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 100
Db 617 VIDKLNVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 659
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## RESULT 5

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US-09-892-949-54
; Sequence 54, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prensell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuipert, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
```

FILE REFERENCE: 00-42  
CURRENT APPLICATION NUMBER: US/09/892,949  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US 60/214,282  
PRIOR FILING DATE: 2000-06-26  
PRIOR APPLICATION NUMBER: US 60/214,955  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/267,963  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: FastSeq for windows Version 3.0  
SEQ ID NO 54  
LENGTH: 662  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-892-949-54

Query Match 50.6%; Score 514.5; DB 11; Length 662;  
Best Local Similarity 94.2%; Pred. No. 8.5e-45;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60  
DB 557 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616  
QY 61 VIDKLNVNFGNVLQEIFTDEARTGOENNLGEGKNG--YVTCG 100  
DB 617 VIDKLNVNFGNVLQEIFTDEARTGOENNLGEGKNGRIIISCP 659

RESULT 6  
US-10-006-265-17  
Sequence 17, Application US/1006265  
Publication No. US20030125520A1  
GENERAL INFORMATION:  
APPLICANT: Maeda, Masatsugu  
APPLICANT: Yasuchi, No. US20030125520A1iko  
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10  
FILE REFERENCE: 06501-096001  
CURRENT APPLICATION NUMBER: US/10/006,265  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: PCT/JP00/03556  
PRIOR FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: JP 11/155797  
PRIOR FILING DATE: 1999-06-02  
PRIOR APPLICATION NUMBER: JP 11/217797  
PRIOR FILING DATE: 1999-07-30  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 17  
LENGTH: 662  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-006-265-17

Query Match 50.6%; Score 514.5; DB 15; Length 662;  
Best Local Similarity 94.2%; Pred. No. 8.5e-45;  
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60  
DB 557 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616  
QY 61 VIDKLNVNFGNVLQEIFTDEARTGOENNLGEGKNG--YVTCG 100  
DB 617 VIDKLNVNFGNVLQEIFTDEARTGOENNLGEGKNGRIIISCP 659

RESULT 7  
US-09-972-708-12  
Sequence 12, Application US/09972708  
Publication No. US20030059871A1  
GENERAL INFORMATION:

APPLICANT: Immunex Corporation  
APPLICANT: Cosman, David J.  
APPLICANT: Mosley, Bruce A.  
APPLICANT: Bird, Timothy A.  
APPLICANT: Dubose, Robert F.  
APPLICANT: Wiley, Steven R.  
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
FILE REFERENCE: 3160-B  
CURRENT APPLICATION NUMBER: US/09/972,708  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 726  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-972-708-12

Query Match 47.5%; Score 483.5; DB 11; Length 726;  
Best Local Similarity 56.0%; Pred. No. 1.6e-41;  
Matches 107; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 1 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60  
DB 541 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 597  
QY 61 VIDKLNVNFGNVLQEIFTDEARTGOENNLGEGKNGVTCPPRPPDCLGKSPFELVSPER 120  
DB 598 LIDKLNVNFGNVLQEIFTDEARTGOENNLGEGKNGVTCPPRPPDCLGKSPFELVSPER 657  
QY 121 PPKSQYLRSNPECTREPAKEQLLFGSOS--LYVDHLCEGAPNPYLKNSVTAREFLVS 178  
DB 658 ASEDSHSTCSRADAVSELRARQPSGSCSPSPSPR--EDQAQNPYIKNSVTAREFLVS 715  
QY 179 EKLPEHTGGEV 189  
DB 716 ENIPHSKGEV 726

RESULT 8  
US-09-972-708-14  
Sequence 14, Application US/09972708  
Publication No. US20030059871A1  
GENERAL INFORMATION:  
APPLICANT: Immunex Corporation  
APPLICANT: Cosman, David J.  
APPLICANT: Mosley, Bruce A.  
APPLICANT: Bird, Timothy A.  
APPLICANT: Dubose, Robert F.  
APPLICANT: Wiley, Steven R.  
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
FILE REFERENCE: 3160-B  
CURRENT APPLICATION NUMBER: US/09/972,708  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 652  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-972-708-14

Query Match 45.4%; Score 462; DB 11; Length 652;  
Best Local Similarity 100.0%; Pred. No. 2.4e-39;  
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60  
DB 557 KKPNTLTHLCPVTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616  
QY 61 VIDKLNVNFGNVLQEIFTDEARTGOE 86  
DB 617 VIDKLNVNFGNVLQEIFTDEARTGOE 642

## RESULT 9

US-10-006-265-2  
; Sequence 2, Application US/10006265  
; Publication No. US20030125520A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masaatsu  
; APPLICANT: Yaguchi, No. US20030125520A1ko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10  
; FILE REFERENCE: 06501-096001  
; CURRENT APPLICATION NUMBER: US/10/006,265  
; PRIOR FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: PCT/JP00/03556  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: JP 11/155797  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: JP 11/217797  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 652  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-265-2

Query Match 45.4%; Score 462; DB 15; Length 652;  
Best Local Similarity 100.0%; Pred. No. 2,4e-39;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKKNKTLTLCMPVPNPAESSIATWGGDDPKDKLNKESDVSNTEDRIKPCSTPSDKL 60  
DB 557 KKKNKTLTLCMPVPNPAESSIATWGGDDPKDKLNKESDVSNTEDRIKPCSTPSDKL 616

QY 61 VIDKLNVNFGNVLOEIFTDEARTGOE 86  
DB 617 VIDKLNVNFGNVLOEIFTDEARTGOE 642

## RESULT 10

US-09-892-949-57  
; Sequence 57, Application US/09892949  
; Publication No. US20030096339A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Fresnell, Scott R.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Kujper, Joseph L.  
; APPLICANT: Maurer, Mark F.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
; FILE REFERENCE: 00-42  
; CURRENT APPLICATION NUMBER: US/09/892,949  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,282  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,955  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/267,963  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 57  
; LENGTH: 662  
; TYPE: PRT  
; ORGANISM: mus musculus  
US-09-892-949-57

Query Match 29.9%; Score 304; DB 11; Length 662;  
Best Local Similarity 58.5%; Pred. No. 6,9e-23;  
Matches 62; Conservative 14; Mismatches 26; Indels 4; Gaps 3;

QY 1 KKKNKTLTLCMPVPNPAESSIATWGGDDPKDKLNKESDVSNTEDRIKPCSTPSDKL 60  
DB 558 KKKNKTLTLCMPVPNPAESSIATWGGDDPKDKLNKESDVSNTEDRIKPCSTPSDKL 614

QY 61 VIDKLNVNFGNVLOEIFTDEARTGOENNIGKNGYVTCPPDPD 106  
DB 615 VIDKLNVNFGNVLOEIFTDEARTGOENNIGKNGYVTCPPDPD 659

## RESULT 11

US-10-190-435-5  
; Sequence 5, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; FILE REFERENCE: P18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 854  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: TV2.12-5/1  
US-10-190-435-5

Query Match 9.4%; Score 95.5; DB 12; Length 854;  
Best Local Similarity 22.3%; Pred. No. 0.5;

Matches 52; Conservative 26; Mismatches 76; Indels 79; Gaps 13;

QY 7 TLCCWPTVPNPAE-----SSIATWGGDDPKDKLNKESDVSNTEDRIKPC--STP 56  
DB 69 TLCCWPTVPNPAE-----SSIATWGGDDPKDKLNKESDVSNTEDRIKPC--STP 123

QY 57 SDKLVIDKLNVNFGNVLOEI-----FTDEARTGOENN-----LGEKNGYV-- 97  
DB 124 CVTLNCTATVATVYNTSDMKKCSFYVTELDKDKKENALFYRLDIYPLNNRKNGLINN 183

QY 98 -----TCTPRPDPLGKSGFELVSPERIP---PKTSQYLR-----SRMPE 134  
DB 184 YRLNCTATVATVYNTSDMKKCSFYVTELDKDKKENALFYRLDIYPLNNRKNGLINN 242

QY 135 GTRPEAKGQLPSGQSLVVDHLCGAGNPVYKNSVTAREPLV-SEKLPEHTK 186  
DB 243 GTRPEAKGQLPSGQSLVVDHLCGAGNPVYKNSVTAREPLV-SEKLPEHTK 275

## RESULT 12

US-10-190-435-128  
; Sequence 128, Application US/10190435  
; Publication No. US20030143248A1  
; GENERAL INFORMATION:  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: BARNETT, Susan W.  
; APPLICANT: LIAN, Ying  
; APPLICANT: ENGELBRECHT, Susan  
; APPLICANT: VAN RENSBURG, Estrelita J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
; FILE REFERENCE: P18133.003 / 2302-18133  
; CURRENT APPLICATION NUMBER: US/10/190,435  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 128

LENGTH: 854  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TV002c12.1  
US-10-190-435-128

Query Match  
Best Local Similarity 22.3%; Score 95.5; DB 12; Length 854;  
Pred. No. 0.5;  
Matches 52; Conservative 26; Mismatches 76; Indels 79; Gaps 13;

QY 7 TLHCPTVNPAAE-----SSATWGGDDFKDKLNKESDVSNTEDRIKPC--STP- 56  
DB 69 THACVPTDPNPOEIVLENTENFMNMK--NDVWDOM-----QEDIIISLMDQSLKPCVLTPL 123  
QY 57 SDKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 97  
DB 124 CCTLNCTATVNNNTSKMKKCSFYVTTTLMDKKKKENALPRLDIVFLNRRKNINNN 183  
QY 98 -----TCPFRPDCPLGKSFELPVSPRIP--PRKSQYLR-----SRMPE 134  
DB 184 YRLINCNTPSAITQAC-KVSPFPIPIHYCAPAGYAPLCKNNKKFNGIGPCDNVSTVQCTH 242  
QY 135 GTRPEAKQLFSGQSLVDPDHLCEBAGAPRYLKNSVTAREFLV-SEKLEPHRTK 186  
DB 243 GIKPVVSTQLLNG-----SLAEEELIIRSENLTNNYK 275

RESULT 13  
US-09-891-609-4  
Sequence 4, Application US/09891609  
Patent No. US20020127238A1  
GENERAL INFORMATION:  
APPLICANT: Stamatacos, Leonidas  
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR  
FILE REFERENCE: 2570-1-002N  
CURRENT APPLICATION NUMBER: US/09/891,609  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: 60/214,608  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 619  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-891-609-4

Query Match  
Best Local Similarity 24.9%; Score 91.5; DB 10; Length 619;  
Pred. No. 0.83;  
Matches 47; Conservative 23; Mismatches 66; Indels 53; Gaps 10;

QY 7 TLHCPTVNPAAE-----ATWGGDDFKDKLNKESDVSNTEDRIKPC--STP- 62  
DB 43 THACVPTDPNPOEIVLENTENFMNMK--NDVWDOM-----QEDIIISLMDQSLKPCVLTPL 99  
QY 63 DKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 107  
DB 100 TLHCPTVNPAAE-----ATWGGDDFKDKLNKESDVSNTEDRIKPC--STP- 150  
QY 108 GKSFEELPVSPRIP-----PRK-----SOYLSRMEGRTPEAKQLFSGQSL 151  
DB 151 KVSFPIPIHYCAPAGYAPLCKNNKKFNGIGPCDNVSTVQCTH 208  
QY 152 VPDHLCERG 160  
DB 209 ----LAERG 213

RESULT 14  
US-09-891-609-2  
Sequence 2, Application US/09891609  
Patent No. US20020127238A1

GENERAL INFORMATION:  
APPLICANT: Stamatacos, Leonidas  
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR  
FILE REFERENCE: 2570-1-002N  
CURRENT APPLICATION NUMBER: US/09/891,609  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: 60/214,608  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 2  
LENGTH: 646  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-891-609-2

Query Match  
Best Local Similarity 24.9%; Score 91.5; DB 10; Length 646;  
Pred. No. 0.88;  
Matches 47; Conservative 23; Mismatches 66; Indels 53; Gaps 10;

QY 7 TLHCPTVNPAAE-----ATWGGDDFKDKLNKESDVSNTEDRIKPC--STP- 62  
DB 70 THACVPTDPNPOEIVLENTENFMNMK--NDVWDOM-----QEDIIISLMDQSLKPCVLTPL 126  
QY 63 DKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 107  
DB 127 TLHCPTVNPAAE-----ATWGGDDFKDKLNKESDVSNTEDRIKPC--STP- 177  
QY 108 GKSFEELPVSPRIP-----PRK-----SOYLSRMEGRTPEAKQLFSGQSL 151  
DB 178 KVSFPIPIHYCAPAGYAPLCKNNKKFNGIGPCDNVSTVQCTH 235  
QY 152 VPDHLCERG 160  
DB 236 ----LAERG 240

RESULT 15  
US-10-190-435-140  
Sequence 140, Application US/10190435  
Publication No. US20030143248A1  
GENERAL INFORMATION:  
APPLICANT: ZUR MEGDE, Jan  
APPLICANT: BARNETT, Susan W.  
APPLICANT: LIAN, Ying  
APPLICANT: ENGELBRECHT, Susan  
APPLICANT: VAN RENSBURG, Estrelita J.  
TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C  
FILE REFERENCE: P18133.003 / 2302-18133  
CURRENT APPLICATION NUMBER: US/10/190,435  
CURRENT FILING DATE: 2002-12-30  
NUMBER OF SEQ ID NOS: 319  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 140  
LENGTH: 865  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TV008c4.3  
US-10-190-435-140

Query Match  
Best Local Similarity 24.7%; Score 88.5; DB 12; Length 865;  
Pred. No. 2.7;  
Matches 38; Conservative 21; Mismatches 48; Indels 47; Gaps 8;

QY 7 TLHCPTVNPAAE-----SSATWGGDDFKDKLNKESDVSNTEDRIKPCSTPSDK 59  
DB 70 THACVPTDPNPOEIVLENTENFMNMK--NDVWDOM-----QEDIIISLMDQSLKPCVLTPL 120  
QY 60 LVIDKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 119  
DB 121 LTPCLVTINCSVIVSNVTNTVT--HNNT--TDKEMNCTFN-----ITTE 164

Qy 120 I PPKSQYLRSRMPEGTREPEAKEQLPFGQSLVP 153  
Db 165 ITDKKS-----KEYATFYRLDVVP 183

Search completed: August 18, 2003, 13:33:23  
Job time : 26.0245 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:23:02 ; Search time 26.4869 Seconds

(without alignments)  
686.221 million cell updates/sec

Title: US-09-892-949-2\_COPY\_544\_732

Perfect score: 1017

Sequence: 1 KKPNTLTHLCPMTVPNPAES.....VTAREPLVSEKLPHTKGEV 189

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length DB | ID     | Description         |
|------------|-------|-------------|-----------|--------|---------------------|
| 1          | 96.5  | 9.5         | 856       | A44963 | env polypeptide pr  |
| 2          | 93    | 9.1         | 918       | A44257 | interleukin-6 sign  |
| 3          | 92.5  | 9.1         | 407       | AB0137 | diethylolipamide S  |
| 4          | 87.5  | 8.6         | 852       | T12016 | envelope glycoprot  |
| 5          | 87    | 8.6         | 495       | S31493 | env polypeptide -   |
| 6          | 86.5  | 8.5         | 548       | T33172 | hypothetical prote  |
| 7          | 86    | 8.5         | 409       | H83448 | diethylolipamide s  |
| 8          | 86    | 8.5         | 846       | VCLJND | env polypeptide pr  |
| 9          | 86    | 8.5         | 853       | S54384 | envelope polypept   |
| 10         | 86    | 8.5         | 861       | VCLJSC | env polypeptide pr  |
| 11         | 85.5  | 8.4         | 1258      | JC5765 | inositol polyphosp  |
| 12         | 84.5  | 8.3         | 718       | AB1258 | hypothetical prote  |
| 13         | 84    | 8.3         | 856       | A53503 | B-lymphocyte-induc  |
| 14         | 83.5  | 8.2         | 358       | JC6121 | transcription fact  |
| 15         | 83.5  | 8.2         | 722       | VCPV2  | coat protein VPI -  |
| 16         | 82.5  | 8.1         | 729       | VCLJX  | env polypeptide pr  |
| 17         | 82.5  | 8.1         | 790       | A35797 | probable DNA-bind   |
| 18         | 82.5  | 8.1         | 861       | VCLJKB | env polypeptide pr  |
| 19         | 82.5  | 8.1         | 917       | I49639 | glycoprotein 130 -  |
| 20         | 81.5  | 8.0         | 358       | A49511 | transcription fact  |
| 21         | 81.5  | 8.0         | 365       | JC1168 | transcription fact  |
| 22         | 81.5  | 8.0         | 855       | VCLJZR | env polypeptide pr  |
| 23         | 81    | 8.0         | 847       | T09448 | envelope glycoprot  |
| 24         | 80    | 7.9         | 467       | A49377 | fibronectin-binding |
| 25         | 80    | 7.9         | 861       | VCLJTV | involucrin - mouse  |
| 26         | 79.5  | 7.8         | 539       | H72422 | env polypeptide pr  |
| 27         | 79.5  | 7.8         | 539       | H72422 | hypothetical prote  |
| 28         | 79.5  | 7.8         | 539       | H72422 | hypothetical prote  |
| 29         | 79.5  | 7.8         | 1355      | T32092 | hypothetical prote  |

|    |      |     |      |   |        |                    |
|----|------|-----|------|---|--------|--------------------|
| 30 | 79   | 7.8 | 423  | 2 | B86214 | hypothetical prote |
| 31 | 79   | 7.8 | 771  | 2 | T38616 | hypothetical prote |
| 32 | 79   | 7.8 | 938  | 2 | T39006 | related to yeast z |
| 33 | 78.5 | 7.7 | 2298 | 2 | T49648 | hypothetical prote |
| 34 | 78   | 7.7 | 358  | 1 | S25464 | transcription fact |
| 35 | 78   | 7.7 | 665  | 2 | UC7191 | 85K c-Cbl-interact |
| 36 | 78   | 7.7 | 713  | 2 | AC3220 | catalase C (import |
| 37 | 78   | 7.7 | 856  | 1 | VCLJ3W | env polypeptide pr |
| 38 | 78   | 7.7 | 960  | 2 | S54461 | hypothetical prote |
| 39 | 77.5 | 7.6 | 971  | 2 | T43656 | matrig-type switch |
| 40 | 77.5 | 7.6 | 1270 | 2 | T09194 | adaptor protein in |
| 41 | 77   | 7.6 | 303  | 2 | T51000 | probable multiubiq |
| 42 | 77   | 7.6 | 1336 | 2 | T02736 | probable SCARCROW  |
| 43 | 77   | 7.6 | 1876 | 2 | E97944 | zinc metalloprotei |
| 44 | 77   | 7.6 | 6831 | 2 | A88852 | protein unc-22 (im |
| 45 | 77   | 7.6 | 6839 | 2 | S57242 | twitcln (similar)  |

#### ALIGNMENTS

##### RESULT 1

A44963 env polypeptide precursor - human immunodeficiency virus type 1 (isolate Z321)

N:Alternate names: coat polypeptide

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 28-May-1999

C:Accession: A44963

R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, C.

AIDS Res. Hum. Retroviruses 5, 121-129, 1989

A>Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: m

A:Reference number: A44963; MUID:89228766; PMID:2713163

A:Accession: A44963

A:Molecule type: DNA

A:Residues: 1-856 <SR1>

A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polypeptide

C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-520/Product: coat protein gp120 #status predicted <CP1>

F:521-856/Product: coat protein gp41 #status predicted <CP2>

F:684-705/Domain: transmembrane #status predicted <TMN>

F:87,132,138,152,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611

Query Match 9.5%; Score 96.5; DB 1; Length 856;

Best Local Similarity 24.9%; Pred. No. 1.6;

Matches 49; Conservative 20; Mismatches 71; Indels 57; Gaps 10;

7 THLCMPVTPNPAESSI--ATMHGDPKQKLNKESDVSUNTEDRIKPC--STP----- 56

DB 70 THACVPTDNPFOELSLGVNTEKFDWMKNNMVEQMHEDVISLMDQSLKPCVKLTPICVTL 129

57 SSKVIVDKLVNFGVNLQ-----IFDPAKTCQ-----NNLGGK 93

DB 130 CNIITKQNTVDTMKEIKNCSYNNMTTELRDKRKIYSLFPLRLIVPIGNSNGDS 189

94 NGY--VTC---PFRDCELGKSFEEPLVSPETIPKSOYLRSRME----- 134

DB 190 SKYRLINCNTSLITQACF-KVSFEIPIH-VCAPIAGFALIKCRDSEFGKGCRCRVSTVQ 247

QY 135 ---GTRPEAKQLFSG 148

DB 248 CTHGIRPVVSTQLING 264

##### RESULT 2

A44257 interleukin-6 signal transducing molecule gp130 - rat

C:Species: Rattus norvegicus (Norway rat)



Db 104 CTDNMGN-----YTVKRRNYTSGGEMKEMKGN-----CSF 134

## RESULT 6

T33172 hypothetical protein M01B12.5 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T33172

R:Becker, M.; Graves, T.; Ozersky, P.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid M01B12.

A:Reference number: 221297

A:Accession: T33172

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-548 <BEC>

A:Cross-references: EMBL:AF067624; PIDN:ACI7564.1; GSPDB:GN00019; CESP:M01B12.5

A:Experimental source: strain Bristol N2; clone M01B12

C:Genetics:

A:Gene: CESP:M01B12.5

A:Map position: 1

A:Intons: 39/1; 70/1; 94/1; 122/3; 190/2; 260/2; 301/3; 372/2

Query Match 8.5%; Score 86.5; DB 2; Length 548;

Best Local Similarity 26.6%; Pred. No. 7.2;

Matches 50; Conservative 29; Mismatches 78; Indels 31; Gaps 9;

QY 15 PNPASSIAT--WHGDDFKDLNLKESDSVN-TEDRIKPCSPSKLVTKLVNFG 70

Db 85 PNAANRLVDERHADTSEDRKRKVKRADRAVEQVL---DPRTLVFRLLQR-G 139

QY 71 NVLQGE---IFTDGA-----RTGOENNLG-----GKNGVYTCFRRDPCPLGKSF 111

Db 140 TILNIDGICSTKEANVYHATGNDLAIKIYKTSILTFKDERRYVTGFRFRHGYCKSN 199

QY 112 EELPVSPETIPPKRSQYLRSMEGTRPEAKQQLFSGQSLVPDHLCEBAPNPYLKNSVT 171

Db 200 PRKQVA--VMAEKEMRNILARMEHVGLPVRKPHLL-KGHVLVWDFLQKQWPAFLKNAL 256

QY 172 AREPLVSE 179

Db 257 SQEVAISK 264

RESULT 7

H83448 dihydrolipoamide succinyltransferase (B2 subunit) PA1586 [imported] - *Pseudomonas aerugi-*

C:Species: *Pseudomonas aeruginosa*

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: H83448

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br-

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Iim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho-

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83448

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <STO>

A:Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AA04975.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: sucB, PA1586

C:Superfamily: dihydrolipoamide acetyltransferase, lipoyl/biotin-binding homology

Query Match 8.5%; Score 86; DB 2; Length 409;

Best Local Similarity 31.9%; Pred. No. 5.4;

Matches 30; Conservative 15; Mismatches 33; Indels 16; Gaps 5;

QY 12 PTPV-NPASSIATWHGDDFKDLNLKESDSVNTEDRIKPCSPSKLVTKLVNFG 70

Db 8 PTFPSVADGTVATWH-----KKRGAVRKDELIV---DIETKVLVEVLAAADG 54

## RESULT 8

T33172 env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

A:Accession: J00066

R:Spire, B.; Site, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;

Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunc

A:Reference number: J00065; MUID:90034200; PMID:2806917

A:Accession: J00066

A:Molecule type: DNA

A:Residues: 1-846 <SPI>

A:Cross-references: GB:M27323; NID:G328154; PIDN:AAA44873.1; PID:G328162

A>Note: the authors translated the codon GCG for residue 523 as Arg

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F.1-29/Domain: signal sequence #status predicted <SIG>

F.30-501/Product: coat protein gp120 #status predicted <CPI>

F.502-846/Product: coat protein gp41 #status predicted <CP2>

F.874-692/Domain: transmembrane #status predicted <TM2>

F.87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 8.5%; Score 86; DB 1; Length 846;

Best Local Similarity 20.2%; Pred. No. 14;

Matches 49; Conservative 23; Mismatches 74; Indels 96; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWHGDDFKDLNLKESDSVNTEDRIKPCSPSKLVTK 64

Db 70 THACVPTDPNPQETLELVNTENFMNWKNNVMEQHMEDIIISLDQSLKXC-----VKLTP 123

QY 65 LVNFGANVLQELFTDEARTGQBNNLGKNGVYTCFRR----- 102

Db 124 LCVTLN-----CTDELNNSKNGKCRVEEBEKKRKCFSVVRDRREQVALFYKLDIVPIDN 177

QY 103 -----PDCPLGKSFEEIPLVSPETIPPKRSQYLRSR----- 131

Db 178 NNRNTSTVRLINCSTSTTTQACP-KISFEPLPIH-PCAPAGFALKRDKKFNQTGPCS 235

QY 132 -----MBEGTRPEAKQQLFSGQSLVPDHLCEBAPNPYLKNSVTAREFLV-SKRLPEH 184

Db 236 NVSTVQCTHGIRPVVSTQLLNG-----SLAEEIIRSENLTNN 275

QY 185 TK 186

Db 276 VK 277

RESULT 9

S54384 envelope polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999

C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377

A:Accession: S54384

A>Status: preliminary

A;Molecule type: genomic RNA  
A;Residues: 1-853 <THR>  
A;Cross-references: EMBL:M2639, NID:g329377, PIDD:AAA45370.1, PID:g329385  
C;Superfamily: type B retrovirus env polypeptide  
C;Keywords: polypeptide

|                       |                  |                |            |             |
|-----------------------|------------------|----------------|------------|-------------|
| Query Match           | 8.5%;            | Score 86;      | DB 2;      | Length 853; |
| Best Local Similarity | 20.8%;           | Pred. NO. 14;  |            |             |
| Matches 49;           | Conservative 28; | Mismatches 81; | Indels 78; | Gaps 10     |

```

QY 7 THLCAPTYENPRESS--ATMGDDPKDKLNKESDQSVNTEBRILKPCSTPDKLV---61
Db 70 THACVPTDNPQOEIIELENTENFNMRKNRVQGMEDDIIISLDQSLKPCYKLPPLCVLTAN 129
QY 62 -IDKLNVNF---GNVLOEI-----FTDEARTGOENNIG 91
Db 130 CIDEVMENTMKNNVNTEIRMKNSCFNITTVVRDKTQVHALFYRLDIYPIIDNDSUNS 189
QY 92 EKNGIVTCT--PFRDCLPGKFEELPVSELPRLPKRSQYLRS-----131
Db 190 TNYRLINCTSAITQACP-KVSFEPIPIH-YCAPAGFALLCKDCKRFNGTGPCTNVSTVO 247
QY 132 MPEGRPEAKELLPSGOSLVFVDHLCBEGAPNLYLNKSTAFRELV-SELTPEHTK 186
Db 248 CTHGIRPVVSTDLLNG-----SLAEETIIRSERVLNNAK 283

```

RESULT 10  
VCLJSC

N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Gutorg, C., Guo, H.G., Franchini, G., Aldovini, A., Collalti, E., Farrell, K., Wong-Staal,  
Virology 164, 531-536, 1988  
A>Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: B28922; MUID:88219542; PMID:13365091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
C:Genetics:  
A:Gene: env  
C:Superfamily: type B retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane proteprotein  
F:1-39/Domains: signal sequence #status predicted <SIG>  
F:1-39/Domains: signal sequence #status predicted <SIG>  
F:87-861/Product: env polyprotein #status predicted <DEP>  
P:87-129,133,140,143,159,163,187,198,224,241,262,276,295,301,302,333,340,356,362,386,396

|    |                       |   |               |       |                                 |
|----|-----------------------|---|---------------|-------|---------------------------------|
|    | Query Match           | 8.5%  | Score 86;     | DB 1; | Length 861;                     |
|    | Best Local Similarity | 29.6%;  | Pred. No. 14; |       |                                 |
|    | Matches               | 29;   | Conservative  | 19;   | Mismatches 42; Indels 8; Gaps 4 |
| Oy | 7                     | THLCWPTVNPRESSI--ATWGDDPKDLNLKESDQSVNTEDRIILPCSPGDKLVIDK    | 64            |       |                                 |
|    |                       | : : : : : : : : : : : :                                     |               |       |                                 |
| Dd | 70                    | THACVPDPENPGEVYGVNTEINFNMKNNKNVEQMHHDIISLMDQSLKPCV---KLTPLC | 125           |       |                                 |
|    |                       | : : : : : : : : : : : :                                     |               |       |                                 |
| Oy | 65                    | LVMNGVNYQLIEFTDEARFGQENNIGKEKGYYT-CPF                       | 101           |       |                                 |
|    |                       | :                 |               |       |                                 |
| Dd | 126                   | VTLNCTNLNDSTVAINT-TSSNRKMRMGEGEINTCSF                       | 162           |       |                                 |
|    |                       | : : : : : : : : : : : :                                     |               |       |                                 |

```

RESULT 11
JC5765
inositol polyphosphate 5-phosphatase (EC 3.1.3.-) 2 - human
C[Species]: Homo sapiens (man)
C[Date]: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 05-Nov-1999
C[Accession]: JC5765
R[Peases, X.; Delcu, S.; De Smedt, F.; Drayer, L.; Erneux, C.
Biochem. Biophys. Res. Commun. 239, 697-700, 1997
Article: Identification of a second SH2-domain-containing protein closely related to the
A[Reference number: JC5765; MUID:98042455; PMID:9367831

```

A:Accession: J05765  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1258 <PES>  
A:Cross-references: GB:Y14185; NID:g2653423; PIDN:CAA4743.1; PID:g1188709; PID:g2653424  
C:Comment: This enzyme plays a role in metabolism of inositol phosphate and phosphatidy/  
C:Superfamily: SAM homology; SH2 homology  
C:Keywords: phosphoric monoester hydrolyase  
F:21-117/Domain: SH2 homology <SH2>  
F:421-729/Domain: catalytic #status predicted <CAT>  
F:927-1171/Region: proline-rich

|    | 8.4%;   | Score 65.5; | DB 2,         | Length | 1258;      |
|----|---|-------------|---------------|--------|------------|
|    | Best Local Similarity   | 25.3%;      | Pred. No. 26; |        |            |
|    | Matches   | 43;         | Conservative  | 16;    | Mismatches |
|    |   |             |               | 54;    | Indels     |
|    |   |             |               | 57;    | Gaps       |
|    |   |             |               | 9      |            |
| Oy | 29 DFKDKLMLKESDSDVNTEDRIILKECPSPSDDVLIDKLWVNGNVLQELITDEA-----   | 81          |               |        |            |
| Dd | 865 NIKRSMMKVRYPTERLGTRRLRYEMIS-----IDK-----DEAGAKSKAP          | 903         |               |        |            |
| Oy | 82 ---RTGQENNIGEKNGIVTCTPPDPDCPLGSGFEEFLPVSEIIPPKSQYGLASRMGEGRP | 138         |               |        |            |
| Dd | 904 SVSSGSQEPRSGSRKKPAFT---BASCLSLRLFEE--PEKPP-----FTG-RP       | 944         |               |        |            |
| Oy | 139 EAKQQLFGSGSLVPDLHCEGABNPY-----LNSTAAEFLYSEKLP               | 182         |               |        |            |
| Dd | 945 PAPPPAAPRESPLTP-RLKEPGAGEPEGVAAPPNNKSINNDAYYLLEQVP          | 993         |               |        |            |

RESULT 12  
AB1258  
hypothetical protein lmo1466 [imported] - *Listeria monocytogenes* (strain EGD-e)  
C|Species: *Listeria monocytogenes*  
C|Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C|Accession: AB1258  
R|Glaser, P.; Frangell, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blocker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fahl, H.; Jones, L.M.; Karc, U.  
Science 294, 849-852, 2001  
A|Authors: Kretz, J., Kuhn, M., Kunst, F., Kurupkat, G., Madueno, E., Maitournam, A., Maok, C., Schlueder, T., Simoes, N., Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.|Title: Comparative genomics of *Listeria* species.  
A|Reference number: AB1077; MUID:21537279; PMID:11679669  
A|Accession: AB1258  
A|Status: preliminary  
A|Molecule type: DNA  
A|Residues: 1-718 <GLA>  
A|Cross-references: GB:NC\_003210; PIDN:CMC99544.1; PID:gl6410895; GSPDB:GN00177  
A|Experimental source: strain EGD-e  
C|Genetics:  
C|Gene: lmo1466

|                       |        |              |       |                                   |
|-----------------------|--------|--------------|-------|-----------------------------------|
| Query March           | 8.3%:  | Score 84.5:  | DB 2, | length 718;                       |
| Best Local Similarity | 24.9%: | Pred. No.15; |       |                                   |
| Matches               | 49;    | Conservative | 29;   | Mismatches 74; Indels 45; Gaps 11 |

  

|    |     |                   |         |          |       |         |       |       |     |        |      |      |
|----|-----|-------------------|---------|----------|-------|---------|-------|-------|-----|--------|------|------|
| Qy | 1   | KKPNKLTHTLCWPTVNP | PAESSIA | TWGGD    | FDKDL | -NLKESD | S     | YNTED | RI  | LKPCST | PSDK | 59   |
| Db | 123 | KKENK-----        | PAPAP   | TST----- | EDKL  | NLKD    | KLSS- | NVSEK | ITS | NI     | SD   | 164  |
| Qy | 60  | LVIDKL            | VNP     | PGNY     | LOE   | IF      | TDE   | ART   | GE  | NN     | LDG  | ENK  |
| Db | 165 | TLTAKS            | KDP-    | NV       | ME    | DV      | YV    | TE    | VE  | KS     | ME   | KI   |
| Qy | 114 | LPVSP             | PEI     | PP       | RS    | QY      | LR    | SR    | ME  | GT     | R    | PEAK |
| Db | 224 | ALVSV             | YAI     | YP-      | NE    | VY      | DE    | Q     | T   | D      | AR   | RR   |
| Qy | 170 | VTARE             | F----   | LVSE     | KLP   | 162     |       |       |     |        |      |      |
| Db | 273 | ETV               | Q       | L        | K     | L       | H     | L     | D   | G      | K    | M    |

RESULT 13  
A53503  
B-lymphocyte-induced maturation protein 1 - mouse  
N:Alternate names: Blimp-1  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C:Accession: A53503  
R:Turner Jr., C.A.; Mack, D.H.; Davis, M.M.  
Cell 77, 297-306, 1994  
A:Title: Blimp-1, a novel zinc finger-containing protein that can drive the maturation c  
A:Reference number: A53503; MUID:94221646; PMID:8168136  
A:Accession: A53503  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-856 <TUN>  
A:Cross-references: GB:U08185; NID:g474283; PIDN:AAA19252.1; PID:g474284  
i:Keywords: transcription factor, zinc finger

```

Query Match Similarity 8.3%; Score 84; DB 2; length 856;
Best Local Similarity 22.1%; Pared No. 22;
Matches 43; Conservative 33; Mismatches 81; Indels 38; Gaps 9

QY 15 PNPASSIATVHGDDFKDKL-----NLKSDSDS---VNTEDRIILKCGSTPSDKL 60
Db 221 PIPANQELILVMVYCRDPFARILHPYPGELLIVNLQTESNPQOYSEKNEIYKSVPKREY 280
QY 61 VIDKLVMNFGN--VLQELFTDPAK--TQGENNLGSEKNGYVTCPPRP-----DCPLIGKS 110
Db 281 SVKELLIKLSDNSKSKDVIYSRNISEFTLEKMDGGRKNGSPMPYPRVYVIRAPLEPD 340
QY 111 FEELPVSSEIPIPRKSQYL-RSRMPGSTRPEAKEQLLFSGQSLVPHLCCEGAPNPLYLKS 169
Db 341 F--LKQSLAVGMERTYIITHSPLESTTSPSP-----ASSSPQSLKSSSPHSPGNT 391
QY 170 VTAREFLVSEKLPEN 184
Db 392 VSP-----LAPGLPEH 402

```

```

RESULT 14
UC6121
transcription factor Pit-1 - chinook salmon
N/Alternate names: transcription factor GHF-1
C/Species: Oncorhynchus tshawytscha (chinook salmon)
C/Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C/Accession: UC6121; A41928
R/Majumdar, S.; Irwin, D.M.; Elsholtz, H.P.
Proc. Natl. Acad. Sci. U.S.A. 93, 10256-10261, 1996
A/Title: Selective constraints on the activation domain of transcription factor Pit-1.
A/Reference number: UC6121; MUID:96413633; PMID:8816787
A/Accession: UC6121
A/Molecule type: mRNA
A/Residues: 1-358 <MAJ>
A/Cross-references: GB:U55045; NID:91621540; PIDN:MAE17254.1; PID:91621541
R:Elsholtz, H.P.; Majumdar-Somlyai, S.; Xiong, F.; Gong, Z.; Hew, C.L.
Mol. Endocrinol. 6, 515-522, 1992
A/Title: Phylogenetic specificity of prolactin gene expression to conservation of Pit-1
A/Reference number: A41928; MUID:92261606; PMID:1350055
A/Accession: A41928
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 198-341 <ELS>
C/Genetics:
A/Gene: pit-1
C/Superfamily: transcription factor Pit-1; homeobox homology; POU domain homology
C/Keywords: DNA binding; homeobox; nucleus; pituitary; transcription regulation
F:199-266/Domain: POU domain homology <POU>
F:283-339/Domain: homeobox homology <HOK>

```

|                       |        |                |        |                |
|-----------------------|--------|----------------|--------|----------------|
| Query Match           | 8.2%;  | Score 83.5;    | DB 1;  | Length 358;    |
| Best Local Similarity | 25.3%; | Pred. No. 7.7; |        |                |
| Matches               | 42;    | Conservative   | 15;    | Mismatches 58; |
|                       |        |                | Indels | 51;            |
|                       |        |                | Gaps   | 7;             |

```

Oy 45 TEERILKPESTSDKVIDKVVNNGVNIJOEIFTEDEATGGENNLGGKXGVCPRPD 104
Db 110 SOTRIIQTOSTVPHPMN-----VNCANTLQCSLAPCLCYOEHGJG-----GS 152
Oy 105 CPLGKSFEEIP---VSPETP--PRKSYLARSMEG-----TRPEAKQLIFS----- 147
Db 153 CSLSHFPPLPAVLTSEBSPLAGNKDOLKLRSPDPDDPPMDSFOIRELEKRPANDFKLRI 212
Oy 148 -----GOSLVPDH-----LCEEGAPNPLYKSVYAREPL 176
Db 213 KLGVTQTVNGEALAAVHGSEFSQTTICRPFMLQLSPKACTIKAIL 258

```

```

RESULT 15
VCPV2
coat protein VP1 - parvovirus H1
C:Species: parvovirus H1
A:Note: host Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Apr-1994
C:Accession: A03699
R:Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A:Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybridization
A:Reference number: A03695; PMID:83112183; PMID:6823009
A:Accession: A03699
A:Molecule type: DNA
A:Residues: 1-722 <RHO>
A:Cross-references: EMBL:X01457; EMBL:J02198
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

```

|                       |        |               |       |                |
|-----------------------|--------|---------------|-------|----------------|
| Query Match           | 8.2%;  | Score 83.5;   | DB 1; | Length 722;    |
| Best Local Similarity | 20.8%; | Pred. No. 19; |       |                |
| Matches               | 43;    | Conservative  | 25;   | Mismatches 82; |
|                       |        |               |       | Indels 57;     |
|                       |        |               |       | Gaps 8         |

  

|    |     |   |                                     |     |
|----|-----|---|-------------------------------------|-----|
| Qy | 4   | NKLTLCWPTVPNPASSI----   | ATWGDGDFDKDLTKESDSVNTEDRLIKPCS----- | 54  |
|    |     |   | :::                                 |     |
| Db | 197 | SRLLTGMPESEYCGVTVHNNQTGHGTIKYKGN----                          | AYDTHQOIWTPMSLVDA                   | 249 |
| Qy | 55  | -----TPSDKLVIDLTV--VNFQVNLQEIFTEARTQENNLGSE-----              | KRGVYTC-                            | 99  |
|    |     |   | :::                                 |     |
| Db | 250 | AMGWVQPSDMQFIQNSMSLNLDBLSDELPRVYVKVYTBQGGGQAIKRYNNDLTACM      |                                     | 309 |
| Qy | 100 | -----PRPDCPLGKSFEEELVPSPEIP-----                              | PRKSQYLRSMEPEGR--                   | 137 |
|    |     |   | :::                                 |     |
| Db | 310 | MVALDSNNILPTPAAQOTSETLGFYPMKPTAPAPARYYFFMPDROLSTVSSNSAEGTQITD |                                     | 369 |
| Qy | 138 | -----PEAKEQQLFSQGSVLVPHDLCEEG                                 | 160                                 |     |
|    |     |   | :::                                 |     |
| Db | 370 | TIGEPQALNSQEPFTIENTLPTLLRTG                                   | 396                                 |     |

Search completed: August 18, 2003, 13:31:22  
Job time : 27.4869 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

```
Run on:      August 18, 2003, 13:13:27 ; Search time 14.3658 Seconds
              (without alignments)
              618.695 Million cell updates/sec
```

Title: US-09-892-949-2\_COPY\_544\_732  
Perfect score: 1017

Sequence: 1 KKPNNKLTHTLCPVTPNPAES.....VTAREFLVSEKLPEHTKGEV 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 96.5  | 9.5         | 856    | 1  | ENV_HV12H   |
| 2          | 93    | 9.1         | 918    | 1  | IL6B_RAT    |
| 3          | 92    | 9.0         | 250    | 1  | HXB9_HUMAN  |
| 4          | 90.5  | 8.9         | 853    | 1  | ENV_HV1E    |
| 5          | 90.5  | 8.9         | 867    | 1  | ENV_HV1J3   |
| 6          | 86    | 8.5         | 846    | 1  | ENV_HV1ND   |
| 7          | 86    | 8.5         | 853    | 1  | ENV_HV122   |
| 8          | 86    | 8.5         | 856    | 1  | ENV_HV15C   |
| 9          | 85    | 8.4         | 380    | 1  | TGT_CLORE   |
| 10         | 84    | 8.3         | 856    | 1  | PREDI_MOUSE |
| 11         | 83.5  | 8.2         | 722    | 1  | COAT_PAVHH  |
| 12         | 83    | 8.2         | 852    | 1  | ENV_HV153   |
| 13         | 82.5  | 8.1         | 790    | 1  | TNP3_HUMAN  |
| 14         | 82.5  | 8.1         | 853    | 1  | ENV_HV1MF   |
| 15         | 82.5  | 8.1         | 861    | 1  | ENV_HV1XB   |
| 16         | 82.5  | 8.1         | 917    | 1  | IL6B_MOUSE  |
| 17         | 81.5  | 8.0         | 358    | 1  | PIT1_ONCKE  |
| 18         | 81.5  | 8.0         | 365    | 1  | PIT1_ONCKE  |
| 19         | 81.5  | 8.0         | 855    | 1  | ENV_HV126   |
| 20         | 81    | 8.0         | 709    | 1  | SHPI_RAT    |
| 21         | 80.5  | 7.9         | 855    | 1  | ENV_HV10Y   |
| 22         | 80    | 7.9         | 467    | 1  | INVO_MOUSE  |
| 23         | 80    | 7.9         | 709    | 1  | SHPI_MOUSE  |
| 24         | 80    | 7.9         | 836    | 1  | GCGR_HUMAN  |
| 25         | 80    | 7.9         | 861    | 1  | ENV_HV1IR   |
| 26         | 79    | 7.8         | 848    | 1  | ENV_HV1IR   |
| 27         | 79    | 7.8         | 1562   | 1  | YFRD_SCHPO  |
| 28         | 78    | 7.7         | 590    | 1  | MSP_TRELE   |
| 29         | 78    | 7.7         | 665    | 1  | SHPI_HUMAN  |
| 30         | 78    | 7.7         | 847    | 1  | ENV_HV151   |
| 31         | 78    | 7.7         | 856    | 1  | ENV_HV1M1   |
| 32         | 78    | 7.7         | 960    | 1  | YMX6_YEAST  |
| 33         | 77.5  | 7.6         | 379    | 1  | PROB_VIBVU  |

## ALIGNMENTS

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| 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | </ |
|----|----|----|----|----|----|----|----|----|----|----|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|----|

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 96909 MW; 839683F8BBBD174E CRC64;

Query Match 9.5%; Score 96.5; DB 1; Length 856;  
 Best Local Similarity 24.9%; Pred. No. 1.1; Indels 57; Gaps 10;

Matches 49; Conservative 20; Mismatches 71; Indels 57; Gaps 10;  
 QY 7 THLCPTVPNPASSI--ATWGGDFPKDKLTKESDSDVNTEDRLKPC--STP-----56  
 DB 70 THACVFPDPNPQELSLGNTVEKEFKDMKNVGEHEDVLSLMDQSLKPCVKLPLCVTLIS 129  
 QY 57 SDKLIVDKLVNNGVNLQF-----IFPDEARTGQF-----NNLGEK 93  
 DB 130 CHNITIKDNTNTVDTEKEEIKKCSYVMTLELDKOKIYSLFRLDLYVIGGSSNGDS 189  
 QY 94 NGY--VTC--PPRPDPLKSFEEFLVSPFIPRKSQYLRSMPF-----134  
 DB 190 SKRLRLCMTSALTQACP-KVSEFPPIPIH-YCAPAGAILKCDDEBEKGKPCRNSTVQ 247  
 QY 135 ---GTRPEAKEQLLFSG 148  
 DB 248 CTGIGIRPVSTQLLNG 264

RESULT 2  
 IL6B RAT STANDARD; PRT; 918 AA.  
 ID IL6B RAT  
 AC PA0190;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (interleukin 6 signal transducer) (Membrane glycoprotein 130) (GP130).  
 GN IL6ST.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=liver.  
 RX MEDLINE=93052397; Pubmed=1427893;  
 RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;  
 RT Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule, gp130.";  
 RL Genomics 14:666-672(1992).  
 CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,

CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN  
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).  
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS AND ENDOTHELIAL CELLS.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 5 fibronectin type III domains.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL; M92340; -; NOT ANNOTATED\_CDS.  
 CC  
 CC PIR; A44257; A44257.  
 DR HSSP; P40189; 1BOU.  
 DR InterPro; IPR002986; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hemtopoptn\_L\_P2.  
 DR Pfam; PF00041; fn3; 3.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS01353; HEMATOPO REC L\_P2; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;  
 KW Repeat.

FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.  
 FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 619 640 POTENTIAL.  
 FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 124 120 IG-LIKE C2-TYPE.  
 FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 222 333 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.  
 FT DOMAIN 724 754 SER-RICH.  
 FT DISULFID 28 54 By similarity.  
 FT DISULFID 48 103 By similarity.  
 FT DISULFID 134 144 By similarity.  
 FT DISULFID 172 181 By similarity.  
 FT DISULFID 457 465 By similarity.  
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 918 AA; 102450 MW; 9818B6FEFF087F7 CRC64;

Query Match 9.1%; Score 93; DB 1; Length 918;  
 Best Local Similarity 22.7%; Pred. No. 2.5;  
 Matches 58; Conservative 28; Mismatches 72; Indels 98; Gaps 14;

QY 11 WPTVPNPASSIATW-----HGDFDKL--NLKESDSD--VNTEDRLKPCSTPDKL 60  
 DB 651 WPNVDPSPSHIAQWSPHTPRHNPNNSKQDMQSDANFTDVSVVEIENNNKPC--PDDLK 708  
 QY 61 VIDKLIVNNGVNLQRIFTDE--ARTGOENNIGG-----EKN-----94  
 DB 709 SLID-----LFLKEKISTGHSAGIGSCSSSRSSISENEBAOSTASTV 756  
 QY 95 ---GVYTCFPRDPCPLGKSF-----ELLP-----VSPFIPRKSQYL 129

Db 757 QYSTVHSGYRHOVSVQVFSRSESTOPLDSEEREDIDQLVDSVDSGELLPRQGYFKQ 816  
 Qy 130 SRNPESTRPE-----AKEQLLFSGQSLVDHLCERGAPNPKNSVTARF- 175  
 Db 817 SCGQCPASPDVSHFGRSSQVPSGSEEDFVRLKQGVSDHISE-----P/-GSEQRRLQ 869  
 Qy 176 --LVSEKLPBHTKGEV 189  
 Db 870 EGSVADALGTGTGQI 885

RESULT 3  
 HXB9 HUMAN  
 ID HXB9 HUMAN STANDARD; PRT; 250 AA.  
 AC P17482; Q9H111;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-FEB-2003 (Rel. 42, Last annotation update)  
 DE Homeobox protein Hox-B9 (Hox-2E) (Hox-2.5).  
 GN HOXB9 OR HOX2E.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;  
 RT "A complete mutation analysis panel of human HOX genes."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Muscle;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdn T.B., Toshiyuki S., Carninci P., Prange C.J.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Mair M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE OF 173-250 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=89378558; PubMed=2570724;  
 RA Giampaolo A., Acampora D., Zappavigna V., Pannese M.,  
 RA D'Esposito M., Care A., Faiella A., Scornaiuolo A., Russo G.,  
 RA Simeone A., Boncinelli E., Peschle C.;  
 RT "Differential expression of human HOX-2 genes along the anterior-  
 RT posterior axis in embryonic central nervous system";  
 RL Differentiation 40:191-197(1989).  
 RN [4]  
 RP SEQUENCE OF 185-250 FROM N.A.  
 RX MEDLINE=90215256; PubMed=2576652;  
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
 RA Gaudino G., Scornaiuolo A., Cafiero M., Faiella A., Simeone A.;  
 RT "Organization of human class I homeobox genes";  
 RL Genome 31:745-756(1989).  
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT  
 CC 5-9 WEEKS FROM CONCEPTION.  
 CC -!- SIMILARITY: BELONGS TO THE ABD-B HOMEBOX FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AY014296; AAG42144.1; -  
 CC EMBL; AY014295; AAG42144.1; JOINED.  
 CC EMBL; BC015565; AAH15565.1; -  
 CC EMBL; X16172; CA342294.1; -  
 CC FIR; A37042; A37042.  
 CC HSSP; P02833; 9ANT.  
 CC TRANSFAC; T01738; -  
 CC Genew; HGNC:5120; HOXB9.  
 CC MIM; 142964; -  
 CC GO; GO:0005634; C:nucleus; NAS.  
 CC GO; GO:0003700; F:transcription factor activity; NAS.  
 CC GO; GO:0007275; P:development; NAS.  
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.  
 CC InterPro; IPR001356; Homeobox.  
 CC InterPro; IPR000047; HTH\_lambdarepressor.  
 CC Pfam; PF00046; homeobox\_1.  
 CC Pfam; PF04617; Hox9\_act; 1.  
 CC PRINTS; PR00024; HOMEBOX.  
 CC PRINTS; PR00031; HTHREPRESSR.  
 CC Prodom; PD000010; Homeobox; 1.  
 CC SMART; SM00389; HOX; 1.  
 CC PROSITE; PS00027; HOMEBOX\_1; 1.  
 CC PROSITE; PS00071; HOMEBOX\_2; 1.  
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 CC Transcription regulation.  
 CC FT DNA BIND 185 244 HOMEBOX.  
 CC FT CONFLICT 173 173 T -> A (IN REF. 3).  
 CC FT SEQUENCE 250 AA; 28058 MW; F06ECB08FBBD2C CXC64;  
 CC SQ

Query Match 9.0%; Score 92; DB 1; Length 250;  
 Best Local Similarity 21.6%; Pred. NO. 0.6;  
 Matches 38; Conservative 27; Mismatches 57; Indels 54; Gaps 8;

Qy 40 DSVNTEPRILKPCSTPSDKLVYDKLVNFGVNLQETTDARTGQENNLGGEKNGYTC 99  
 Db 13 DSIHSEEDAPPAKPSGQ-----YASSRQFHAHL-----EPSC 50  
 Qy 100 PRPDCPL-GKSFELPVSP-----IPPKSQYLSRMEPTGRPEAK 141  
 Db 51 SFQPAVPFGASW--APLSPHAGSLPSVTHPIYPOGVPPAESRYLTWTLEPPARGENA 108  
 Qy 142 EQLLFGQSLV-----PDHLCERGAPNPKNSVTARELVSEKLPBHTKGEV 189  
 Db 109 PG--QGQAAYVAEPLGAPGLKGTPEVSLETS-AGREAVLSNQPGVDNNTI 160

RESULT 4  
 ENV HVLEL  
 ID ENV HVLEL STANDARD; PRT; 853 AA.  
 AC P04581;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11689;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA MEDLINE=6245056; Pubmed=2424612;  
 RX Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;  
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis  
 of two isolates from African patients.";  
 RL Cell 46:63-74(1986).  
 CC -----  
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 CC -----  
 DR EMBL; K03454; AAA44329.1; -;  
 DR EMBL; A07108; CAA00616.1; -;  
 DR HIV; K03454; ENV\$SEI.  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW Aids; Coat protein; glycoprotein; glycoprotein; Transmembrane;  
 KW Signal.  
 FT CHAIN 1 31 BY SIMILARITY.  
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 853 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 154 BY SIMILARITY.  
 FT DISULFID 219 248 BY SIMILARITY.  
 FT DISULFID 229 240 BY SIMILARITY.  
 FT DISULFID 297 330 BY SIMILARITY.  
 FT DISULFID 376 442 BY SIMILARITY.  
 FT DISULFID 383 416 BY SIMILARITY.  
 FT CARBOHYD 87 416 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 853 AA; 96721 MW; F9C0864DAAD07A5 CRC64;  
 Query Match 8.9%; Score 90.5; DB 1; Length 853;  
 Best Local Similarity 22.3%; Pred. No. 3.8;  
 Matches 49; Conservative 21; Mismatches 63; Indels 87; Gaps 10;

QY 7 THLCPTVPNPASSI--ATWHDGDFKOKLNKESDSDVNTEDRLKPCSTPSDKLVYDK 64  
 Db 70 THACVPTDNPDEIALENTVENFNMKNMVMQWHEDIISLWDQSLKFC-----VKLTP 123  
 QY 65 LVVNGNVQLFPTPEARG--QENNNGEKKNQVYTCPP-----RPD 104  
 Db 124 LCVTLN-----CSBELRNNGTMGNVTEEGKMKNCSPNVTTLVKDKKQOYVALPYRLD 177  
 QY 105 -----CPLKSFEEELPVSPEIPPRKSQYLRSR----- 131  
 Db 178 IYVINDSTNSTNRLINCNTSALTQACP-KVSTFEPPIH-YCAPAGRAILKCKDKFN 235  
 QY 132 -----MPEGTPEAKEQLLFSQSLVPHLCEE 159  
 Db 236 GTGPCTNVSTVQCTHGIRPVSSTQLLNGS-----LAEE 269  
 RESULT 5  
 ID ENV\_HV1J3 STANDARD; PRT; 867 AA.  
 AC P12489;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane  
 DE glycoprotein (GP120), Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HIV-1).  
 OS Viruses; Retrod virus; Retroviridae; Lentivirus.  
 OC NCBI\_Taxid=11694;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89352108; Pubmed=2669897;  
 RX Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;  
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of  
 RT HIV-1 and their expression in bacteria.";  
 RL Aids Res. Hum. Retroviruses 5:411-419(1989).  
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 CC -----  
 DR EMBL; M21138; AA03526.1; -;  
 DR HIV; M21138; ENV\$H3.  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW Aids; Coat protein; glycoprotein; glycoprotein; Transmembrane;  
 KW Signal.  
 FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 217 BY SIMILARITY.  
 FT DISULFID 125 208 BY SIMILARITY.  
 FT DISULFID 130 160 BY SIMILARITY.  
 FT DISULFID 230 259 BY SIMILARITY.  
 FT DISULFID 240 251 BY SIMILARITY.  
 FT DISULFID 308 342 BY SIMILARITY.  
 FT DISULFID 388 457 BY SIMILARITY.  
 FT DISULFID 395 450 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 867 AA; 98399 MW; 5F231014688E8680 CRC64;

Query Match 8.9%; Score 90.5; DB 1; Length 867;  
 Best Local Similarity 22.7%; Pred. No. 3.9;  
 Matches 46; Conservative 28; Mismatches 60; Indels 69; Gaps 10;

QY 7 TLHCWPTVNPASSIATWHDGDFKDKLNKES-----DSVNTEDRIKPC-STPS 57  
 DB 70 THACVPTDPNPEVLE-----ENVTKEFNMKNMKNWQMHMEDIIISLMDQSLKCVLTP- 123  
 QY 58 DKLVIDKLVNFEVNGEIEFTDEARTGOENNLGE-KNGVYVTPRPDCLGKSFEELEY 116  
 DB 124 --LCVTLCIDWGNDSPTNATNTTSGGKEMKEMKN-----CSF----- 162  
 QY 117 SPEIPRKSQYLRSMEPTGRPEAKQLFSGQSLVDHLCBEGAPNPKNSVTAREFL 176  
 DB 163 -----NITTSIRDKV-----QKHALFYKRDVPIIN-----NSTKMNKNKDNSTRYL 205  
 QY 177 VS-----EKLPEH 184  
 DB 206 ISCNTSVITQACPKISFEPIPIH 228

RESULT 6  
 ID ENV\_HVIND STANDARD; PRT; 846 AA.  
 AC P18799;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11695;

RA MEDLINE=90034200; Pubmed=2806917;  
 RA Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,  
 RA Hampe A., Chermann J.C.;  
 RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the  
 RT human immunodeficiency virus.";  
 RL Gene 81:275-284(1989).  
 CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH  
 CC AIDS. AND IS A HIGHLY CYTOPATHOGENIC STRAIN.

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DR EMBL; M27323; AAA44873.1; -;  
 DR PIR; J00066; VCLJND.  
 DR HIV; M27323; ENV5NDK.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW Aids; Coat protein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT CHAIN 1 29  
 FT DISULFID 30 501  
 FT DISULFID 52 846  
 FT DISULFID 53 73  
 FT DISULFID 118 200  
 FT DISULFID 125 191  
 FT DISULFID 130 152  
 FT DISULFID 213 242  
 FT DISULFID 223 234  
 FT DISULFID 291 328  
 FT DISULFID 374 435  
 FT DISULFID 381 408  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 151 151  
 FT CARBOHYD 179 179  
 FT CARBOHYD 182 182  
 FT CARBOHYD 229 229  
 FT CARBOHYD 236 236  
 FT CARBOHYD 257 257  
 FT CARBOHYD 271 271  
 FT CARBOHYD 284 284  
 FT CARBOHYD 290 290  
 FT CARBOHYD 351 351  
 FT CARBOHYD 382 382  
 FT CARBOHYD 388 388  
 FT CARBOHYD 392 392  
 FT CARBOHYD 395 395  
 FT CARBOHYD 401 401  
 FT CARBOHYD 438 438  
 FT CARBOHYD 451 451  
 FT CARBOHYD 452 452  
 FT CARBOHYD 601 601  
 FT CARBOHYD 606 606  
 FT CARBOHYD 615 615  
 FT CARBOHYD 627 627  
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2EB83 CRC64;

Query Match 8.5%; Score 86; DB 1; Length 846;  
 Best Local Similarity 20.2%; Pred. No. 9.2;  
 Matches 49; Conservative 23; Mismatches 74; Indels 96; Gaps 9;

QY 7 TLHCWPTVNPASSI--ATWHDGDFKDKLNKESDSDVNTEDRIKPCSTSDKLVIDK 64  
 DB 70 THACVPTDPNPEVLE-----ENVTKEFNMKNMKNWQMHMEDIIISLMDQSLKCVLTP- 123  
 QY 65 LVVNFENVNGEIEFTDEARTGOENNLGKNGVYVTPFR----- 102  
 DB 124 LCVTLCIDWGNDSPTNATNTTSGGKEMKEMKN-----CSF----- 162  
 QY 103 -----PDCLGKSFEELEPVSEPIPRKSYLRSS----- 131  
 DB 178 NNRRTSTNYRLINCSTSTTQACP-KISEPIPIH-FCAPAFALIKCDKFKNGTGPS 235  
 QY 132 -----MPGRTPEAKQLFSGQSLVDHLCBEGAPNPKNSVTAREFLV-SKLPKH 184  
 DB 236 NVSTWQCTGIRPVVSTOLLNG-----SLAEEIITRSENLTN 275  
 QY 185 TK 186



FT SITE 760 760 IN-FRAME TERMINATION CODON.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 160 BY SIMILARITY.  
 FT DISULFID 219 247 BY SIMILARITY.  
 FT DISULFID 228 239 BY SIMILARITY.  
 FT DISULFID 296 330 BY SIMILARITY.  
 FT DISULFID 376 439 BY SIMILARITY.  
 FT DISULFID 383 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97055 MW; DAFADA600BA7A08 CRC64;

Query Match 8.5%; Score 86; DB 1; Length 856;  
 Best Local Similarity 29.6%; Pred. No. 9.3;  
 Matches 29; Conservative 19; Mismatches 42; Indels 8; Gaps 4;  
 QY 7 THLCWPTVNPASSI--ATWGDGDFKDKLNLKESDVSNTEDRIILKPCSTPDKLVIDK 64  
 DB 70 THACVPIIDPRQGVVIGVNTENMMKNNVQGMHEDIIISLMQSLKPCV----KILPLC 125  
 QY 65 LVVNFQVNLQEIITDEARFGQENNLGGEKNGVYT-CPE 101  
 DB 126 VTLNCTNLNRDSTINATNT-TSSNRGMEGEGWNTNCSF 162

RESULT 9  
 TGT\_CLOPE  
 ID TGT\_CLOPE STANDARD; PRT; 380 AA.  
 AC 08XJ16;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE transglycosylase (EC 2.4.2.29) (tRNA-guanine  
 transferase)  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OC NCBI\_TaxID=1502;  
 RN 11  
 RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 flesh-eater."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).  
 CC -1- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-  
 deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His  
 and -Tyr). After this exchange, a cyclopentimidic moiety is  
 attached to the 7-aminomethyl group of 7-deazaguanine, resulting  
 in the hypermodified nucleoside quenosine (Q) (7-((4,5-cis-  
 dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By  
 similarity).  
 CC -1- CATALYTIC ACTIVITY: tRNA guanine + guanine = tRNA guanine +  
 guanine.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE QUEUINE tRNA-RIBOSYLTRANSFERASE FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL, AP00192; BAB81651.1; -.  
 DR HAMAP, MF\_00168; -; 1.  
 DR InterPro, IPR004803; QtrRNA\_ribo\_trans.  
 DR InterPro, IPR002616; tRNA\_ribo\_trans.  
 DR Pfam, PF01702; TGT, 1.  
 DR TIGRPFAM, TIGR00430; Q tRNA tgt; 1.  
 DR TIGRPFAM, TIGR00449; tgt\_general; 1.  
 KW Quenosine biosynthesis; transferase; glycosyltransferase;  
 KW tRNA processing; zinc; complete proteome.  
 KW ACT SITE 94  
 FT ACT SITE 276 276 BY SIMILARITY.  
 FT METAL 313 313 ZINC (BY SIMILARITY).  
 FT METAL 315 315 ZINC (BY SIMILARITY).  
 FT METAL 318 318 ZINC (BY SIMILARITY).  
 FT METAL 344 344 ZINC (BY SIMILARITY).  
 SQ SEQUENCE 380 AA; 43200 MW; BOB7CA1D254BED8 CRC64;

Query Match 8.4%; Score 85; DB 1; Length 380;  
 Best Local Similarity 25.8%; Pred. No. 4.1;  
 Matches 33; Conservative 19; Mismatches 40; Indels 36; Gaps 5;  
 QY 14 VNPNA-----ESSIA---TWGDDPFKDKLNLKESDVSNTEDRIILKPCSTPDKLVIDK 65  
 DB 150 INPSTRREVESVARTIRMLERCKKEMDRNLSDDTYRKQMLG----- 195  
 QY 66 VVNFQVNLQEIITDEARFGQENNLGGEKNGVYT-CPEPDKPKGKSPFEL-----PVSPET 120  
 DB 196 -INQGGVEDIRIEHAKTIREMDLDGYAIGIA-----VGETHEMYRVIDAIVPHL 246  
 QY 121 PPKSGOYL 128  
 DB 247 PEDKPIYL 254

RESULT 10  
 PRD1\_MOUSE  
 ID PRD1\_MOUSE STANDARD; PRT; 856 AA.  
 AC Q60636;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE PR-domain zinc finger protein 1 (beta-interferon gene positive-  
 regulatory domain 1 binding factor) (BLIMP-1).  
 GN PRDM1 OR BLIMP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/c;  
RX MEDLINE=94221646; PubMed=8168136;  
RA Turner C.A., Mack D.H., Davis M.M.;  
RT "Blimp-1, a novel zinc finger-containing protein that can drive the  
RT maturation of B lymphocytes into immunoglobulin-secreting cells.",  
RL Cell 77:297-306(1994).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=20572522; PubMed=11121475;  
RA Tunayapin C., Shapiro M.A., Calame K.L.;  
RT "Characterization of the B lymphocyte-induced maturation protein-1  
RT (Blimp-1) gene, mRNA isoforms and basal promoter.";  
RL Nucleic Acids Res. 28:4846-4851(2000).  
CC -1- FUNCTION: Transcriptional repressor that binds specifically to the  
CC PRD1 element in the promoter of the beta-interferon gene. Drives  
CC the maturation of B lymphocytes into Ig secreting cells.  
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).  
CC -1- SIMILARITY: Contains 1 SET domain.  
CC -----  
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CC -----  
DR EMBL; U08185; AAA19252.1; -  
DR EMBL; AF305539; AAC42212.1; -  
DR EMBL; AF305534; AAC42212.1; JOINED.  
DR EMBL; AF305535; AAC42212.1; JOINED.  
DR EMBL; AF305536; AAC42212.1; JOINED.  
DR EMBL; AF305537; AAC42212.1; JOINED.  
DR EMBL; AF305538; AAC42212.1; JOINED.  
DR PIR; A51503; A51503.  
DR HSSP; P08048; 72NF.  
DR TRANSFAC; T02316; -  
DR MGD; MGI:96655; Ptdml.  
DR InterPro; IPR001214; SET.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR Pfam; PF008856; SET; 1.  
DR Pfam; PF00886; Zf\_C2H2; 5.  
DR ProDom; PD000003; Znf\_C2H2; 1.  
DR SMART; SM00317; SET; 1.  
DR SMART; SM00355; Znf\_C2H2; 4.  
DR PROSITE; PS00280; SET; 1.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
KW Transcription regulation; Repressor; DNA-binding; Zinc-finger;  
KW Metal-binding; Nuclear protein; Repeat.  
FT DOMAIN 118 237 SET.  
FT ZN\_FING 606 628 C2H2-TYPE.  
FT ZN\_FING 634 656 C2H2-TYPE.  
FT ZN\_FING 662 684 C2H2-TYPE.  
FT ZN\_FING 690 712 C2H2-TYPE.  
SQ SEQUENCE 856 AA; 95835 MW; B9AC6FC2E29ECF4A CRC64;  
Query Match 8.3%; Score 84; DB 1; Length 856;  
Best Local Similarity 22.1%; Pred. No. 14;  
Matches 43; Conservative 33; Mismatches 81; Indels 38; Gaps 9;  
QY 15 PNEASSIATWHDGDFKDL-----NLESKSDS---VNTEDRIKPCSTPSDKL 60  
DB 221 PIRANGELIWMYCRDFERLHYRYPGELIVINLTQTESNPKOYSSSEGNELYPSSVKKREY 280  
QY 61 VIDKLIVNFGN--VLQEIFTDEAR--TGQENNIAGEKNGYVTCPPRP-----DCPLGKS 110  
DB 281 SVKEILLIDENPSKRKDIYRSNISPTLEKMDGFRKNGSPDMFPYRVVYPIRALPLED 340

QY 111 FEELVPSPEIPPRKSOYL-RSRMPEGTPEAKEQLFSGQSLVPHLCEGAPNPLYKNS 169  
DB 341 F--LKASLAVGMERPTIYHSPISSTPSPP-----ASSSPQSLKSSSPHSPGNT 391  
QY 170 VTAREFLVSEKPEH 184  
DB 392 VSP---LAPGLPEH 402  
RESULT 11  
ID COAT\_PAVH STANDARD; PRT; 722 AA.  
AC P03136;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Coat protein VP1 (Contains: Coat protein VP2).  
OS Hamster parvovirus H1.  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=10799;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83112183; PubMed=6823009;  
RA Rhode S.L. III, Paradiso P.R.;  
RT "Parvovirus genome: nucleotide sequence of H-1 and mapping of its  
RT genes by hybrid-arrested translation.";  
RL J. Virol. 45:173-184(1983).  
CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES COAT PROTEIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; X01457; CAB57285.1; ALT\_SEQ.  
DR PIR; A03699; VCPV2.  
DR HSSP; P07302; 1MW4.  
DR InterPro; IPR001403; Parvo\_coat.  
DR Pfam; PF00740; Parvo\_coat; 1.  
KW Coat protein; Glycoprotein.  
FT CHAIN 1 722  
FT CARBOHYD 178 722 COAT PROTEIN VP1.  
FT CARBOHYD 178 722 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 647 647 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DOMAIN 155 170 GLY-RICH  
SQ SEQUENCE 722 AA; 79737 MW; 6BB678391A5DC31 CRC64;  
Query Match 8.2%; Score 83.5; DB 1; Length 722;  
Best Local Similarity 20.8%; Pred. No. 12;  
Matches 43; Conservative 25; Mismatches 82; Indels 57; Gaps 8;  
QY 4 NKLTLCWFTVNPABSSI---ATWGDGDFKDLNLESKSDSVNTEDRIKPCSTPSDKL 54  
DB 197 SRLTLHGMPSESNYKRVTVNHNQTTGHGTVKGNM-----AYDTHQIIMTPWISLVDA 249  
QY 55 -----TPSDKVIDKLIV--VNFQVLDIEFTDEARTQENNLGGE-----KNGVYTC 99  
DB 250 ANGWFQPSDWDQFIONSWESLWLSQLEFVNVVKTVTBQGAQDALKYNNNDLTACM 309  
QY 100 -----PRPDCPLGKSFEELPVSEIP-----PRKSOYLRSRMPEGTR--- 137  
DB 310 MWALDSNNILPYTPAAQISSETIGFYPWKPTAPAPRYFFPMWRQLSVYSNSABEGQITND 369  
QY 138 ---PEAKQLIFSGQSLVPHLCEEG 160  
DB 370 TIGEPQALNSQFTIENTLPIILRLTG 396



DR SMART; SM00259; ZnF\_A20; 7.  
DR PROSITE; PS00802; OTU; 1.  
KM Apoptosis; DNA-binding; Zinc-finger; Repeat.  
FT DOMAIN 92 263 OTU  
FT REPEAT 286 356 2 X APPROXIMATE REPEATS.  
FT REPEAT 286 317 1.  
FT REPEAT 324 356 2.  
FT DOMAIN 369 775 INTERACTION WITH NAF1 (BY SIMILARITY).  
FT DOMAIN 387 782 ZINC-FINGERS.  
FT ZN\_FING 387 407  
FT ZN\_FING 478 498  
FT ZN\_FING 521 539  
FT ZN\_FING 607 627  
FT ZN\_FING 657 677  
FT ZN\_FING 716 736  
FT ZN\_FING 762 782  
SO SEQUENCE 790 AA; 89613 MW; 320AEA97F58D4491 CRC64;

Query Match 8.1%; Score 82.5; DB 1; Length 790;  
Best Local Similarity 25.6%; Pred. No. 17;  
Matches 33; Conservative 17; Mismatches 48; Indels 31; Gaps 5;

QY 75 EIFTDARTQENNLGEEKKGYTCPPR-----PDCLGKSFELVSPR 119  
DB 347 ELVQHEKMKQENSEQRRREGHAQNPWEPSPVQLSLMDVKCTPNCPEFMSVNTQPLCHE 406  
QY 120 IPRKSO-----YLRSM-PEG-----TRPEAKQLFS-GOSLVDPDLCEGAPY 163  
DB 407 CSRRKQNKMLKLNKSKPEPEGLPKALGASGEATPLANNPESTGSPHAPPTAAS 466  
QY 164 PYLKNVTA 172  
DB 467 PFLFSETTA 475

RESULT 14  
ENV\_HVLMF STANDARD; PRT; 853 AA.  
AC P19551;  
ID ENV\_HVLMF STANDARD; PRT; 853 AA.  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11704;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90317877; PubMed=1695254;  
RA Stevenson M., Haggerty S., Lamonic C., Mann A.M., Meier C.,  
RA Maslak A.;  
RT "Cloning and characterization of human immunodeficiency virus type 1  
RT variants diminished in the ability to induce syncytium-independent  
RT cytolysis."  
RL J. Virol. 64:3792-3803 (1990).  
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CC -----  
CC EMBL; M33943; AAA44850.1; -.  
DR PDB; 1A1K; 16-JUN-97.  
DR HIV; M33943; ENVSMFA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;  
KM 3D-structure.  
FT SIGNAL 1 30  
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 31 509 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 54 74 BY SIMILARITY.  
FT DISULFID 119 203 BY SIMILARITY.  
FT DISULFID 126 194 BY SIMILARITY.  
FT DISULFID 131 157 BY SIMILARITY.  
FT DISULFID 216 245 BY SIMILARITY.  
FT DISULFID 226 237 BY SIMILARITY.  
FT DISULFID 294 329 BY SIMILARITY.  
FT DISULFID 376 443 BY SIMILARITY.  
FT DISULFID 383 416 BY SIMILARITY.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 8.1%; Score 82.5; DB 1; Length 853;  
Best Local Similarity 22.7%; Pred. No. 19;  
Matches 49; Conservative 18; Mismatches 66; Indels 83; Gaps 10;

QY 7 THLCPTVNPAPASSI--ATWHGDDFKLANKESDSDSVNEDRLIKCSTPSDKLVLDK 64  
DB 71 THACVPTDNPPEVILVNTENFDMKMDWQGMHEDILSLMDQSLKNC-----VKLTP 124  
QY 65 LVVFNQNVLOEITFTDEARTGQENNIGG---EKNGVTCPP----- 101  
DB 125 LCVNKK-----CTDLKNDNTNNSNGRMIMKEGIRKCSFNISIRNKQKEYAFYK 178  
QY 102 ---RP-----DCLGKSFELVSPRIPRKSQYLR----- 130  
DB 179 LDIRPLDNTTYRLISCNTSVITQACP-KVSFFPPIIH-YCAPAGRAILKCKNDKTNGTGP 236  
QY 131 -----RMPESTRPEAKQLFSGOSLVDPDLCEH 159  
DB 237 CINVSTVQCTHGRIRPVVSQILLNS-----LAE 266

RESULT 15  
ENV\_HV1KB STANDARD; PRT; 861 AA.  
AC P31819;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)



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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:47 ; Search time 66.8907 Seconds  
(without alignments)  
729.128 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_544\_732

Perfect score: 1017  
Sequence: 1 KKPNTLTHCWPVTVPNPAES.....VTAREFLVSEKLPHTKGGEV 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_23: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp Vertebrate: \*  
14: sp Unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 1017  | 100.0       | 732    | Q8N117 | Q8N117 homo sapien |
| 2          | 483.5 | 47.5        | 716    | Q8K5B1 | Q8K5B1 mus musculu |
| 3          | 479.5 | 47.1        | 235    | Q8BSU3 | Q8BSU3 mus musculu |
| 4          | 479.5 | 47.1        | 716    | Q8R501 | Q8R501 mus musculu |
| 5          | 115   | 11.3        | 801    | Q99BY7 | Q99BY7 human immun |
| 6          | 115   | 11.3        | 801    | Q99BX7 | Q99BX7 human immun |
| 7          | 104.5 | 10.3        | 503    | Q74827 | Q74827 human immun |
| 8          | 104   | 10.2        | 501    | Q75951 | Q75951 human immun |
| 9          | 104   | 10.2        | 501    | Q75939 | Q75939 human immun |
| 10         | 103   | 10.1        | 501    | Q75937 | Q75937 human immun |
| 11         | 103   | 10.1        | 501    | Q75942 | Q75942 human immun |
| 12         | 102.5 | 10.1        | 791    | Q99BX1 | Q99BX1 human immun |
| 13         | 100   | 9.8         | 515    | Q74304 | Q74304 human immun |
| 14         | 99.5  | 9.8         | 865    | Q9QGM8 | Q9QGM8 human immun |
| 15         | 99    | 9.7         | 800    | Q99BY1 | Q99BY1 human immun |
| 16         | 98.5  | 9.7         | 869    | Q91V33 | Q91V33 human immun |

|    |      |     |      |    |        |                    |
|----|------|-----|------|----|--------|--------------------|
| 17 | 98   | 9.6 | 795  | 15 | Q99BX6 | Q99BX6 human immun |
| 18 | 98   | 9.6 | 864  | 15 | Q9E610 | Q9E610 simian-huma |
| 19 | 98   | 9.6 | 871  | 15 | P88155 | P88155 human immun |
| 20 | 97.5 | 9.6 | 788  | 15 | Q99BY6 | Q99BY6 human immun |
| 21 | 97   | 9.5 | 855  | 15 | Q75837 | Q75837 human immun |
| 22 | 97   | 9.5 | 856  | 15 | Q9DS18 | Q9DS18 human immun |
| 23 | 97   | 9.5 | 860  | 15 | Q9E1S6 | Q9E1S6 human immun |
| 24 | 96.5 | 9.5 | 855  | 15 | Q9YKQ4 | Q9YKQ4 human immun |
| 25 | 96.5 | 9.5 | 856  | 15 | Q9Q2G3 | Q9Q2G3 human immun |
| 26 | 96   | 9.4 | 475  | 15 | Q9WR11 | Q9WR11 human immun |
| 27 | 95.5 | 9.4 | 854  | 15 | Q9QMH2 | Q9QMH2 human immun |
| 28 | 95.5 | 9.4 | 855  | 15 | Q9QD15 | Q9QD15 human immun |
| 29 | 95.5 | 9.4 | 857  | 15 | Q9Q0Q6 | Q9Q0Q6 human immun |
| 30 | 95   | 9.3 | 479  | 15 | Q76124 | Q76124 human immun |
| 31 | 95   | 9.3 | 805  | 15 | Q99BY5 | Q99BY5 human immun |
| 32 | 95   | 9.3 | 849  | 15 | Q41803 | Q41803 human immun |
| 33 | 95   | 9.3 | 859  | 15 | P87924 | P87924 human immun |
| 34 | 95   | 9.3 | 1281 | 11 | Q9R1P5 | Q9R1P5 mus musculu |
| 35 | 94.5 | 9.3 | 756  | 15 | Q99BW9 | Q99BW9 human immun |
| 36 | 94.5 | 9.3 | 848  | 15 | Q69988 | Q69988 human immun |
| 37 | 94.5 | 9.3 | 848  | 15 | Q69990 | Q69990 human immun |
| 38 | 94.5 | 9.3 | 856  | 15 | Q72993 | Q72993 human immun |
| 39 | 94.5 | 9.3 | 858  | 15 | Q75114 | Q75114 human immun |
| 40 | 94   | 9.2 | 482  | 15 | Q9WR14 | Q9WR14 human immun |
| 41 | 94   | 9.2 | 794  | 15 | Q99BY3 | Q99BY3 human immun |
| 42 | 94   | 9.2 | 856  | 15 | P90115 | P90115 human immun |
| 43 | 94   | 9.2 | 862  | 15 | Q9WLG8 | Q9WLG8 human immun |
| 44 | 94   | 9.2 | 863  | 15 | Q9Q6H1 | Q9Q6H1 human immun |
| 45 | 93.5 | 9.2 | 529  | 15 | Q77979 | Q77979 human immun |

## ALIGNMENTS

## RESULT 1

Q8N117 PRELIMINARY; PRT; 732 AA.  
ID Q8N117  
AC Q8N117  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Gp130-like monocycle receptor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21988187; PubMed=11877449;  
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;  
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals Proliferation, and Activates STAT-3 and STAT-5.";  
RL J. Biol. Chem. 277:16831-16836(2002).  
DR EMBL; AF486620; AAM27958.1; -  
DR InterPro; IPR002396; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 3.  
KW Receptor.  
SQ SEQUENCE 732 AA; 82953 MW; 30F84BD3DD9A20E CRC64;

Query Match 100.0%; Score 1017; DB 4; Length 732;  
Best Local Similarity 100.0%; Pred. No. 6,2e+89;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | KKPNTLTHCWPVTVPNPAESSIAIWHGDPFKDKLNKESDSSVNTEDRIILKPCSTPSDKL | 60  |
| DB | 544 | KKPNTLTHCWPVTVPNPAESSIAIWHGDPFKDKLNKESDSSVNTEDRIILKPCSTPSDKL | 603 |
| QY | 61  | VIDKLVNFGNVLQEIFDEARTGQENNLGCKNGVYTCPPRPDCLPKSFEELVPSPEI     | 120 |
| DB | 604 | VIDKLVNFGNVLQEIFDEARTGQENNLGCKNGVYTCPPRPDCLPKSFEELVPSPEI     | 663 |

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723  
QY 181 LPEHTKGEV 189  
DB 724 LPEHTKGEV 732

## RESULT 2

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723  
QY 181 LPEHTKGEV 189  
DB 724 LPEHTKGEV 732

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723  
QY 181 LPEHTKGEV 189  
DB 724 LPEHTKGEV 732

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

RC STRAIN=C57BL/6J; TISSUE=pituitary;  
RX MEDLINE=22354683; PubMed=1246851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
RL EMBL; AK030512; BAC26998.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 50928397A1AD126F CRC64;

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 180  
DB 664 PPRKSOYLRSRMPEGRPEAKQQLPSGQSLVPDHLCEBAPNPYLKNSVTAREPLVSEK 723

QY 121 PPRKSYLASMPEGRPEAKBQLFSGOS--LVPHLCBEGANPYLNKSTAREFLVS 178  
DB 648 ASSEDSHSTCSRMADEAYSEIARQPSSSCSQPSLSPR--EDQKONPYLNKSNVTTREFLVH 705  
QY 179 EKLPEHTKGEV 189  
DB 706 ENIPEHSGEV 716

## RESULT 5

Q99BX7 PRELIMINARY; PRT; 801 AA.  
AC Q99BX7; 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
EN Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Suthent R., Sistrupanon S.;  
RT "Biological and immunological characteristics of HIV-1 subtype E in cerebrospinal fluid and blood."  
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF322195; AAK09402.1; -  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 801 801  
SQ SEQUENCE 801 AA; 90874 MW; 25FD3484A1FB1153 CRC64;

Query Match 11.3%; Score 115; DB 15; Length 801;  
Best Local Similarity 24.0%; Pred. No. 0.026;  
Matches 58; Conservative 30; Mismatches 78; Indels 76; Gaps 12;

QY 7 THLCWPTVNPAPSSSI--ATWGGDDPKDKLNKESDVSNTEDRIKPC--STP----- 56  
DB 18 THACVPTDPNPQEMPLKNVTENFMNKKMAEQMEDVLSLMDQSLKPCVKLTPLCVTLTD 77  
QY 57 -----SDKLVIDKLNVNFGVLOEI-----FTDEARFGOE----- 86  
DB 78 CTYANMTTANLTJSDKSNISRII--GNLTBEVRNCSFNMTELRDRQKQVHTLFYKLDIV 134  
QY 87 --NNLGEKNGVYTC--PRPDCPLGKSPFELPVSPBP-----PRK 124  
DB 135 PIDNSNHSKRYRLINCNSNVKQACP-KISFDPIPHYCTPAGYAILKCNKKFNGTGPK 193  
QY 125 SOYLASRMPEGRPEAKBQLFSGOSLVPDHCCEGAPNPYLNKSTAREFLVSEKLPBH 184  
DB 194 -DVSSVQCTHGIRKPVVSTQLVNGS-----LAEEING--KSSRRRIIISSENLTNN 243  
QY 185 TK 186  
DB 244 AK 245

## RESULT 6

Q99BX7 PRELIMINARY; PRT; 801 AA.  
AC Q99BX7; 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
EN Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Suthent R., Sistrupanon S.;  
RT "Biological and immunological characteristics of HIV-1 subtype E in cerebrospinal fluid and blood."  
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF322205; AAK09412.1; -  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 801 801  
SQ SEQUENCE 801 AA; 90833 MW; 04FA14142F6D37A4 CRC64;

Query Match 11.3%; Score 115; DB 15; Length 801;  
Best Local Similarity 24.0%; Pred. No. 0.026;  
Matches 58; Conservative 30; Mismatches 78; Indels 76; Gaps 12;

QY 7 THLCWPTVNPAPSSSI--ATWGGDDPKDKLNKESDVSNTEDRIKPC--STP----- 56  
DB 18 THACVPTDPNPQEMPLKNVTENFMNKKMAEQMEDVLSLMDQSLKPCVKLTPLCVTLTD 77  
QY 57 -----SDKLVIDKLNVNFGVLOEI-----FTDEARFGOE----- 86  
DB 78 CTYANMTTANLTJSDKSNISRII--GNLTBEVRNCSFNMTELRDRQKQVHTLFYKLDIV 134  
QY 87 --NNLGEKNGVYTC--PRPDCPLGKSPFELPVSPBP-----PRK 124  
DB 135 PIDNSNHSKRYRLINCNSNVKQACP-KISFDPIPHYCTPAGYAILKCNKKFNGTGPK 193  
QY 125 SOYLASRMPEGRPEAKBQLFSGOSLVPDHCCEGAPNPYLNKSTAREFLVSEKLPBH 184  
DB 194 -DVSSVQCTHGIRKPVVSTQLVNGS-----LAEEING--KSSRRRIIISSENLTNN 243  
QY 185 TK 186  
DB 244 AK 245

## RESULT 7

Q74827 PRELIMINARY; PRT; 503 AA.  
AC Q74827; 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
EN Envelope glycoprotein gp120 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blouin J.;  
RT Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.  
DR EMBL; U43110; AAA85201.1; -  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 503 503  
SQ SEQUENCE 503 AA; 53F94F51217B1C4A CRC64;

Query Match 10.3%; Score 104.5; DB 15; Length 503;  
Best Local Similarity 23.6%; Pred. No. 0.15;  
Matches 43; Conservative 27; Mismatches 91; Indels 21; Gaps 6;

QY 7 THLCWPTVNPAPSSSI--ATWGGDDPKDKLNKESDVSNTEDRIKPCSTSDKLVIDK 64  
DB 70 THACVPTDPNPQEMPLKNVTENFMNKKMAEQMEDVLSLMDQSLKPCVKLTPLCVTLR 129



OX NCB1\_TaxID=11676;  
 [1] \_SEQUENCE FROM N.A.  
 RC STRAIN=94CV42-10e;  
 RA Gao F., Vidal N., Li Y., Trask S.A., Chen Y., Kostrikis L.G., Ho D.D.,  
 RA Kim J., Choe K., Oh W.-D., Salminen M., Robertson D.L., Shaw G.M.,  
 RA Hahn B.H., Peeters M.;  
 RT "Evidence for two distinct sub-subtypes within the HIV-1 subtype A  
 RT radiation";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF286249; AAK82673.1; -;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 865 AA; 97687 MW; C32E79B7EA71F3C CRC64;

Query Match 9.8%; Score 99.5; DB 15; Length 865;  
 Best Local Similarity 24.1%; Pred. No. 0.89; Indels 65; Gaps 10;  
 Matches 49; Conservative 20; Mismatches 69; Indels 65; Gaps 10;

QY 7 THLCWPTVPNPASSIAVHGDDEKDLNLES--DSSVNTEDRIILKPC----- 53  
 DB 67 THACVPTDPNPQEIHLNVTEDFNMNMKNMVEQMHEDIISLMDQSLKPCVLTPLCVTLN 126  
 QY 54 -----STPSDKL-----VIDKLNVNFGNV-----LOEITDEARTGOEN 87  
 DB 127 CSNANVSSTPNDAISTPPGEIKNSYVVTTERIDKTONVHSLFYRLDVQIDESK--NEN 184  
 QY 88 NLGGEKNKY--VVC---PFRDPCPLGKSPFELPVSPPEIPRKSQYLRSME----- 134  
 DB 185 TSSSSNTMYRLINCNTSTTQACP-KITEPIPIH-YCAPAGFALLKCKDPERNGTGSCK 242  
 QY 135 -----GTRPEAKQQLFSG 148  
 DB 243 NVSSVQCTHGIRKPVVSTQLLNG 265

RESULT 15  
 Q99BY1 PRELIMINARY; PRT; 800 AA.  
 ID Q99BY1  
 AC Q99BY1;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCB1\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sutherland R., Srisurapanon S.;  
 RT "Biological and immunological characteristics of HIV-1 subtype B in  
 RT cerebrospinal fluid and blood";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF322201; AAK09408.1; -;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 800 AA; 90879 MW; BBBFOC3791E2B38C CRC64;

Query Match 9.7%; Score 99; DB 15; Length 800;  
 Best Local Similarity 20.2%; Pred. No. 0.9; Indels 88; Gaps 11;  
 Matches 50; Conservative 32; Mismatches 77; Indels 88; Gaps 11;  
 QY 7 THLCWPTVPNPASSI--ATWHDGDFDKLNLKESDSSVNTEDRIILKPC--STP----- 56

DB 18 THACVPTDPNPQEIHLNVTEDFNMNMKNMVEQMHEDIISLMDQSLKPCVLTPLCVTLN 77  
 QY 57 -----SKLVYDKL--VNVFNVVQEI-----FTD 79  
 DB 78 CVDARKNSNIIKNTDTARIGNITDEVNCSFNMTEIIDKQAYALFYKLDIAPIED 137  
 QY 80 EARTGOENNLGGEKNKYVTC---PFRDPCPLGKSPFELPVSPPEIP----- 121  
 DB 138 DHTISKYNSNENYRLINCNSIITQACP-KISFPIPIHYCTPAGYAILKCNDRNG 196  
 QY 122 PRKSQYLS-RMPEGTRPEAKQQLFSGQSLVPHLCEGAPNPLYLKNSTAREFLV-SE 179  
 DB 197 DRPKNVSSVQCTHGIRKPVVSTQLLNG-----SLAEELIRSE 236  
 QY 180 KLPEHTK 186  
 DB 237 MLTNNAK 243

Search completed: August 18, 2003, 13:30:20  
 Job time : 70.8907 secs

DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
DE (Clone B1BR002M.01052AED) proviral 5' ORF (Fragment).  
GN ENV.  
OC Human immunodeficiency virus 1.  
OS Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Brazil;  
RA Ranjbar S., Holmes H.;  
RT "Molecular Characterization of HIV-1 isolate from Brazil."  
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L35491; AA: A72446.1;  
DR InterPro: IPR007777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 501 501  
SQ SEQUENCE 501 AA; 56427 MW; B6BEC500741883A5 CRC64;

Query Match 10.1%; Score 103; DB 15; Length 501;  
Best Local Similarity 25.3%; Pred. No. 0.2;  
Matches 41; Conservative 24; Mismatches 71; Indels 26; Gaps 8;

QY 7 THLCWPTVNPASSI--ATWHDGDKDLNKLKESDVSNTEDRIKPCSTSDKLVYK 64  
DB 71 THACVPTDNPQVLENTENFNMMKNNVCEQMHEDIISLMDQSLKPC-----VKITP 124  
QY 65 LVNFGNVLQELFTDARTGOENNLGGE-KNGVYTCPPRPDCLGK-----FEELPV 116  
DB 125 ICVTLLN--CSDVNTTNTTSSWENMGELIKN-----CSFNITISIGKVKADVALPRLV 178  
QY 117 SP-EIPPRKQYLRSMPEGTPEAKEQLLFGQSLVPHLC 157  
DB 179 VIDNAKNTTSYMLINCNTSVITQACPISFEP---IPHYC 217

## RESULT 12

Q99BX1 PRELIMINARY; PRT; 791 AA.  
AC Q99BX1; 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sutent R., Sistruppanon S.;  
RT "Biological and immunological characteristics of HIV-1 subtype B in cerebrospinal fluid and blood."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: A632211; AK09418.1;  
DR InterPro: IPR000328; Env GP41.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 791 791  
SQ SEQUENCE 791 AA; 89550 MW; A2C337158E9871FB CRC64;

Query Match 10.1%; Score 102.5; DB 15; Length 791;  
Best Local Similarity 21.3%; Pred. No. 0.41;  
Matches 51; Conservative 34; Mismatches 73; Indels 81; Gaps 13;

QY 7 THLCWPTVNPASSI--ATWHDGDKDLNKLKESDVSNTEDRIKPC--STP----- 56  
DB 18 THACVPTDNPQVLENTENFNMMKNNVCEQMHEDIISLMDQSLKPCVLTPLCTILN 77  
QY 57 -SDKLVIDKLNVN-----FGNVLOEI-----FTDARTGOEN-----NLGE 92

DB 78 CVDANKLNSINIITDEARIGNISDEVNCSFNITTELDKKQKHALFYRLDIYKIGND 137  
QY 93 KNG-----YVTCP---FRDPCPLGKSFEEPLVSPPEIPPRKQYLR----- 130  
DB 138 NNSREYRLINCNSIITQACP-KISFDPIPIH-YCTPAGYAFKCKNDKFKNGTGPCKNVS 195  
QY 131 --RMEGTRPEAKEQLLFGQSLVPHLCCEGAPNPYLKNSVYAEFLV-SEKLPEHTK 186  
DB 196 SVQCTHGKIPVYSTQLLLNG-----SLAEELIIRSENLANNAK 234

## RESULT 13

Q74304 PRELIMINARY; PRT; 515 AA.  
AC Q74304; 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
DE Envelope glycoprotein gp120 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ray S.C., Lubaki N.M., Dhruva B.R., Siliciano R.F., Bollinger R.C.;  
RT "Strain-specific Cytolytic T Lymphocyte responses directed against Human immunodeficiency virus type 1 env."  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L78831; AA: B02635.1;  
DR InterPro: IPR007777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 515 515  
SQ SEQUENCE 515 AA; 57626 MW; 5AF783BA2498A619 CRC64;

Query Match 9.8%; Score 100; DB 15; Length 515;  
Best Local Similarity 23.9%; Pred. No. 0.41;  
Matches 58; Conservative 23; Mismatches 100; Indels 62; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWHDGDKDLNKLKESDVSNTEDRIKPC--STP----- 56  
DB 70 THACVPTDNPQVLENTENFNMMKNNVCEQMHEDIISLMDQSLKPCVLTPLCTILN 129  
QY 57 -SDKLVIDKLNVNFGNVLQELFT-----DEARTGOENNLGGEKKNVYVCP 100  
DB 130 CSDYKNDNTNTEIANCSFNINTNIRKVGQYALFYKIDVVPVIGNDSTRYRLKSCNTSV 189  
QY 101 FRDPCPLGKSFEEPLVSPPEIPPR-----KSQYLRSMPE-----EGTRPEAKEQL 144  
DB 190 ITQACP-KVSEFPIPIHCAAGFALLKCKKFKNGTGPCKNVSIVQCTHGKIPVYSTQL 248  
QY 145 LFGQSLVPHD-----HLCBEGAPNPYLKNSVYAEFLVSEKLPETHK 186  
DB 249 LLNG-SLAEEVVRSENFNTNNAKTIIVQNESVAINCIRNNNTRKSIHIGRAFYTT 307  
QY 187 GEV 189  
DB 308 GEV 310

## RESULT 14

Q90QW8 PRELIMINARY; PRT; 865 AA.  
AC Q90QW8; 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:12:37 ; Search time 9.1214 Seconds  
(without alignments)  
417.649 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_520\_543  
Perfect score: 109  
Sequence: 1 ILITSLIGGGILLITLTVAYGL 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1980.DAT:\*  
2: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1981.DAT:\*  
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4: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1983.DAT:\*  
5: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1984.DAT:\*  
6: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1985.DAT:\*  
7: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1986.DAT:\*  
8: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1987.DAT:\*  
9: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1988.DAT:\*  
10: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1989.DAT:\*  
11: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1990.DAT:\*  
12: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1991.DAT:\*  
13: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1992.DAT:\*  
14: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1993.DAT:\*  
15: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1994.DAT:\*  
16: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1995.DAT:\*  
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20: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA1999.DAT:\*  
21: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA2000.DAT:\*  
22: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA2001.DAT:\*  
23: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA2002.DAT:\*  
24: /SIDSL/gcgdata/geneeq/geneeq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 109   | 100.0       | 581    | 24    | ABP54367    |
| 2          | 109   | 100.0       | 620    | 22    | ABG05070    |
| 3          | 109   | 100.0       | 627    | 24    | ABP54366    |
| 4          | 109   | 100.0       | 649    | 23    | ABG05738    |
| 5          | 109   | 100.0       | 652    | 22    | ABG51242    |
| 6          | 109   | 100.0       | 652    | 23    | AAE24028    |
| 7          | 109   | 100.0       | 662    | 22    | ABG51244    |
| 8          | 109   | 100.0       | 662    | 23    | AAE24029    |
| 9          | 109   | 100.0       | 662    | 23    | ABG05741    |

|    |      |       |     |    |          |
|----|------|-------|-----|----|----------|
| 10 | 109  | 100.0 | 681 | 24 | ABP54363 |
| 11 | 109  | 100.0 | 732 | 23 | ABG05730 |
| 12 | 109  | 100.0 | 745 | 23 | AAE24024 |
| 13 | 109  | 100.0 | 764 | 24 | ABP54364 |
| 14 | 109  | 100.0 | 764 | 24 | ABP54365 |
| 15 | 83   | 76.1  | 662 | 24 | ABG05742 |
| 16 | 83   | 76.1  | 716 | 24 | ABP54370 |
| 17 | 83   | 76.1  | 716 | 24 | ABP54371 |
| 18 | 82   | 75.2  | 726 | 23 | AAE24037 |
| 19 | 52   | 47.7  | 795 | 22 | ABG62996 |
| 20 | 51   | 46.8  | 302 | 23 | ABG03986 |
| 21 | 51   | 46.8  | 318 | 22 | AAU24652 |
| 22 | 51   | 46.8  | 318 | 22 | AAU24652 |
| 23 | 51   | 46.8  | 318 | 23 | ABP95651 |
| 24 | 51   | 46.8  | 318 | 23 | ABJ04725 |
| 25 | 51   | 46.8  | 318 | 23 | AAU95704 |
| 26 | 51   | 46.8  | 318 | 23 | AAU85272 |
| 27 | 51   | 46.8  | 318 | 24 | ABR01682 |
| 28 | 51   | 46.8  | 318 | 24 | ABU11168 |
| 29 | 50   | 45.9  | 314 | 23 | AAE25071 |
| 30 | 50   | 45.9  | 325 | 23 | ABP51564 |
| 31 | 49.5 | 45.4  | 363 | 22 | AAU91861 |
| 32 | 49   | 45.0  | 25  | 18 | AAW34001 |
| 33 | 49   | 45.0  | 92  | 20 | AAW97363 |
| 34 | 49   | 45.0  | 116 | 21 | AAU01911 |
| 35 | 49   | 45.0  | 270 | 23 | ABP95678 |
| 36 | 49   | 45.0  | 313 | 22 | AAU71830 |
| 37 | 49   | 45.0  | 324 | 23 | AAU48227 |
| 38 | 49   | 45.0  | 337 | 15 | AAK53753 |
| 39 | 49   | 45.0  | 337 | 19 | AAW48734 |
| 40 | 49   | 45.0  | 337 | 21 | AAU21698 |
| 41 | 49   | 45.0  | 337 | 23 | AAU91240 |
| 42 | 49   | 45.0  | 352 | 13 | AAU27792 |
| 43 | 49   | 45.0  | 352 | 16 | AAK68812 |
| 44 | 49   | 45.0  | 352 | 16 | AAK80757 |
| 45 | 49   | 45.0  | 352 | 20 | AAU39993 |

## ALIGNMENTS

RESULT 1  
ABP54367  
ID ABP54367 standard; Protein; 581 AA.  
XX  
AC ABP54367;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human NR10.6 splicing variant protein SEQ ID NO:10.  
XX  
KW NR10, splicing variant; haematopoietin receptor; immunomodulator;  
KW haemostatic; haematopoietic factor; immunological disease;  
KW haematopoietic disease; haematopoietic cell regulation.  
XX  
OS Homo sapiens.  
XX  
EN WO200277230-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 22-MAR-2002; 2002WO-JP02769.  
XX  
PR 26-MAR-2001; 2001JP-0087298.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Maeda M, Yaguchi N, Hasegawa M;  
XX  
DR WPI, 2003-018925/01.  
XX  
DR N-PSDB; ABG83367.  
XX  
PT NR10 splicing variants of haematopoietin receptor proteins and encoded

PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
PS Claim 1; Fig 13-15; 250pp; Japanese.  
XX  
CC The present invention describes hematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC hematopoietic factors, and developing remedies for immunological and  
CC hematopoietic diseases. The haematopoietin receptor genes participate  
CC in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.6  
CC protein from the present invention.  
XX  
SQ Sequence 581 AA;  
Query Match 100.0%; Score 109; DB 24; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IILITSLIGGGLLILITLVAYGL 24  
DB 552 IILITSLIGGGLLILITLVAYGL 575  
RESULT 2  
ABG05070  
ID ABG05070 standard; Protein; 620 AA.  
XX  
AC ABG05070;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #5061.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS69257.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID No 35429; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polynucleic acid chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 620 AA;  
Query Match 100.0%; Score 109; DB 22; Length 620;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IILITSLIGGGLLILITLVAYGL 24  
DB 408 IILITSLIGGGLLILITLVAYGL 431  
RESULT 3  
ABP54366  
ID ABP54366 standard; Protein; 627 AA.  
XX  
AC ABP54366;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human NR10.5 splicing variant protein SEQ ID NO:8.  
XX  
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;  
KW haemostatic; hematopoietic factor; immunological disease;  
KW hematopoietic disease; hematopoietic cell regulation.  
XX  
OS Homo sapiens.  
XX  
PN WO200277230-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 22-MAR-2002; 2002WO-JP02769.  
XX  
PR 26-MAR-2001; 2001JP-0087298.  
XX  
PA (CHUS) CHUGAI SEIYAKU KK.  
XX  
PI Maeda M, Yaguchi N, Hasegawa M;  
XX  
DR WPI; 2003-018925/01.  
DR N-PSDB; ABQ83366.  
XX  
XX NR10 splicing variants of haematopoietin receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX  
PS Claim 1; Fig 10-12; 250pp; Japanese.  
XX  
CC The present invention describes hematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC hematopoietic factors, and developing remedies for immunological and  
CC hematopoietic diseases. The haematopoietin receptor genes participate  
CC in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.5  
CC protein from the present invention.  
XX  
SQ Sequence 627 AA;

Query Match 100.0%; Score 109; DB 24; Length 627;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IILITSLIGGGILLIITLVAYGL 24  
 Db 552 IILITSLIGGGILLIITLVAYGL 575

RESULT 4  
 ABB05738  
 ID ABB05738 standard; Protein; 649 AA.

AC ABB05738;  
 DT 01-MAY-2002 (first entry)

DE Human zcytor17 protein sequence SEQ ID NO:46.

KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytosstatic;  
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

PN WO200200721-A2.

PD 03-JAN-2002.

PF 26-JUN-2001; 2001WO-US20484.

PR 26-JUN-2000; 2000US-214282P.

PR 29-JUN-2000; 2000US-214955P.

PR 08-FEB-2001; 2001US-267963P.

PA (ZYMO) ZYMOGENETICS INC.

PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuiper JL;

PI Maurer MF;

DR WPI; 2002-090519/12.

DR N-PSDB; ABA93803.

PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is

PT useful for treating and diagnosing lymphoid, immune, inflammatory,

PT splenic, blood or bone disorders -

PS Claim 18; Page 195-197; 235pp; English.

XX The present invention describes a cytokine receptor designated zcytor17.  
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17  
 CC proteins are useful for treating and diagnosing lymphoid, immune,  
 CC inflammatory, splenic, blood or bone disorders. Agonists or  
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
 CC immunity and for stimulating lymphocyte proliferation, such as in the  
 CC treatment of infections involving immunosuppression, including certain  
 CC viral infections. They are also useful for inducing cytotoxicity and  
 CC for treating leukopenia. Antagonist of zcytor17 polypeptides are useful  
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
 CC exemplification of the present invention.

SO Sequence 649 AA;

Query Match 100.0%; Score 109; DB 23; Length 649;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IILITSLIGGGILLIITLVAYGL 24  
 Db 520 IILITSLIGGGILLIITLVAYGL 543

RESULT 5  
 AAB51242  
 ID AAB51242 standard; Protein; 652 AA.

AC AAB51242;

DT 26-MAR-2001 (first entry)

DE Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.

KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;  
 KW immunoregulation; haematopoietic cell regulation; transmembrane;  
 KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;  
 KW metal allergy; pollen allergy.

OS Homo sapiens.

PN WO200075314-A1.

PD 14-DEC-2000.

PF 01-JUN-2000; 2000WO-JP03556.

PR 02-JUN-1999; 99JP-0155797.

PR 30-JUL-1999; 99JP-0217797.

PA (CHUG) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Maeda M, Yaguchi N;

DR WPI; 2001-061720/07.

DR N-PSDB; AAC92337.

PT Hematopoietin receptor protein NR10 for screening potential ligands for

PT treatment of immune and hematopoietic disorders such as autoimmune

PT diseases and allergies -

PS Claim 1; Fig 3-5; 127pp; Japanese.

XX The present sequence represents a human haemopoietin receptor protein  
 CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane  
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule  
 CC which participates in immunoregulation and haematopoietic cell  
 CC regulation in vivo, and is useful in searching for haematopoietic  
 CC factors capable of binding to the receptor. NR10 can be used for the  
 CC identification of substances for the treatment and prevention of immune  
 CC and haematopoietic disorders including autoimmune diseases and allergies  
 CC such as metal and pollen allergy.

SO Sequence 652 AA;

Query Match 100.0%; Score 109; DB 22; Length 652;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGILLIITLVAYGL 24  
 Db 533 IILITSLIGGGILLIITLVAYGL 556

RESULT 6  
 AAE24028  
 ID AAE24028 standard; Protein; 652 AA.

AC AAE24028;

DT 23-SEP-2002 (first entry)  
 XX  
 DE Human HPRI variant protein #2.  
 XX  
 KW Human; haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;  
 KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
 KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
 KW osteoclast disorder; periodontitis; acute polymyopathy; Bell's palsy;  
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 KW ischaemic disease; variant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200229060-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 05-OCT-2001; 2001MO-US31634.  
 XX  
 PR 06-OCT-2000; 2000US-238706P.  
 PR 13-OCT-2000; 2000US-240476P.  
 PR 20-FEB-2001; 2001US-270282P.  
 XX  
 XX (IMMV) IMMUNEX CORP.  
 XX  
 PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,  
 PI WPI; 2002-330172/36.  
 DR  
 XX Human and murine hematopoietin receptor polypeptides HPRI and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 PT hormone related conditions -  
 XX  
 XX Disclosure; Page 110-112; 136pp; English.  
 PS  
 XX The present invention relates to human and murine hematopoietin receptor  
 CC polypeptides HPRI and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukaemia and tumour  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related conditions. They are useful for treating various hematologic and  
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (SCC and NSCC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC squamous cell carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC sarcoma), cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocy-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such  
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polymyopathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC myasthenia gravis, chronic neuronal degeneration, stroke including  
 CC cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful  
 CC for treating various other disorders such as osteoporosis, obesity,  
 CC deficient mammary development and infertility. The present sequence  
 CC is human HPRI variant protein.  
 CC  
 ,XX

SQ Sequence 652 AA;  
 Query Match 100.0%; Score 109; DB 23; Length 652;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ILITSLIGGGLIITLVAYGL 24  
 DB 533 ILITSLIGGGLIITLVAYGL 556  
 RESULT 7  
 AAB51244  
 ID AAB51244 standard; Protein; 662 AA.  
 XX  
 AC AAB51244;  
 XX  
 DT 26-MAR-2001 (first entry)  
 XX  
 DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.  
 XX  
 KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;  
 KW immunoregulation; haematopoietic cell regulation; transmembrane;  
 KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;  
 KW metal allergy; pollen allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200075314-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 01-JUN-2000; 2000MO-JP03556.  
 XX  
 PR 02-JUN-1999; 99JP-0155797.  
 PR 30-JUL-1999; 99JP-0217797.  
 XX  
 XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 PA  
 XX Maeda M, Yaguchi N;  
 PI WPI; 2001-061720/07.  
 DR N-PSDB; AAC92350.  
 XX  
 PT Hematopoietin receptor protein NR10 for screening potential ligands for  
 PT treatment of immune and hematopoietic disorders such as autoimmune  
 PT diseases and allergies -  
 XX  
 XX Claim 1; Fig 13-14; 127pp; Japanese.  
 PS  
 XX The present sequence represents a human haemopoietin receptor protein  
 CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane  
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule  
 CC which participates in immunoregulation and haematopoietic cell  
 CC regulation in vivo, and is useful in searching for haematopoietic  
 CC factors capable of binding to the receptor. NR10 can be used for the  
 CC identification of substances for the treatment and prevention of immune  
 CC and haematopoietic disorders including autoimmune diseases and allergies  
 CC such as metal and pollen allergy.  
 CC  
 SQ Sequence 662 AA;  
 Query Match 100.0%; Score 109; DB 22; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ILITSLIGGGLIITLVAYGL 24  
 DB 533 ILITSLIGGGLIITLVAYGL 556  
 RESULT 8  
 AAB24029

AAE24029 standard; Protein; 662 AA.  
 AAE24029;  
 23-SEP-2002 (first entry)  
 Human HPR1 variant protein #3.  
 Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;  
 pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
 neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
 cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
 ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
 osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;  
 anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease;  
 demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
 vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
 stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 ischaemic disease; variant.  
 Homo sapiens.  
 MO200229060-A2.  
 11-APR-2002.  
 05-OCT-2001; 2001WO-US31634.  
 06-OCT-2000; 2000US-238706P.  
 13-OCT-2000; 2000US-240476P.  
 20-FEB-2001; 2001US-270282P.  
 (IMMW) IMMUNEX CORP.  
 Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;  
 WPI; 2002-330172/36.  
 Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,  
 useful for treating cell proliferation, metabolic, and reproductive  
 hormone related conditions -  
 Disclosure; Page 112-115; 136pp; English.  
 The present invention relates to human and murine hematopoietin receptor  
 polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 resulting from a lack of bone-forming cells. They are also useful for  
 treating cell proliferation conditions such as leukaemia and tumour  
 metastasis, osteoporosis resulting from an excess of bone-resorbing  
 cells. HPR sequences are also useful for treating medical conditions and  
 diseases such as cell proliferation, metabolic and reproductive hormone  
 related conditions. They are useful for treating various haematologic and  
 oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
 cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
 cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 dysplastic syndromes (including refractory anaemia, refractory anaemia  
 with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 myeloid metaplasia, osteoclast disorders that lead to bone loss such  
 as osteoporosis including post-menopausal osteoporosis, periodontitis  
 resulting in tooth loosening or loss, prosthesis loosening after joint  
 replacement, neurodegenerative conditions (e.g., acute polynuropathy,  
 Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 dementia including Creutzfeld-Jacob disease, demyelinating neuropathy,  
 Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 myasthenia gravis, chronic neuronal degeneration, stroke including  
 cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful

for treating various other disorders such as osteoporosis, obesity,  
 deficient mammary development and infertility. The present sequence  
 is human HPR1 variant protein.  
 SEQ Sequence 662 AA;  
 Query Match 100.0%; Score 109; DB 23; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ILLITSLGGGILLITITVAYGL 24  
 533 ILLITSLGGGILLITITVAYGL 556  
 RESULT 9  
 ABB05741  
 ID ABB05741 standard; Protein; 662 AA.  
 AC ABB05741;  
 DT 01-MAY-2002 (first entry)  
 DE Human zcytor17 protein sequence SEQ ID NO:54.  
 KW zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;  
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.  
 OS Homo sapiens.  
 PN WO200200721-A2.  
 PD 03-JAN-2002.  
 PF 26-JUN-2001; 2001WO-US20484.  
 PR 26-JUN-2000; 2000US-214282P.  
 PR 29-JUN-2000; 2000US-214955P.  
 PR 08-FEB-2001; 2001US-267963P.  
 XX (ZWO) ZWONEMENTICS INC.  
 XX Sprecher CA, Preenell SR, Gao Z, Whitmore TE, Kuiper JL;  
 PI Maurer MF;  
 DR WPI; 2002-090519/12.  
 DR N-PSDB; ABA93808.  
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
 PT splenic, blood or bone disorders -  
 PS Example 1; Page 204-206; 235pp; English.  
 XX The present invention describes a cytokine receptor designated zcytor17.  
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17  
 CC proteins are useful for treating and diagnosing lymphoid, immune,  
 CC inflammatory, splenic, blood or bone disorders. Agonists or  
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
 CC immunity and for stimulating lymphocyte proliferation, such as in the  
 CC treatment of infections involving immunosuppression, including certain  
 CC viral infections. They are also useful for inducing cytotoxicity and  
 CC for treating leukopneias. Antagonist of zcytor17 polypeptides are useful  
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
 CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to  
 CC chromosome 5, specifically to the Sg11 chromosomal region. ABA93767 to  
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the

CC exemplification of the present invention.  
XX  
SQ Sequence 662 AA;

Query Match 100.0%; Score 109; DB 23; Length 662;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILILITVAYGL 24  
Db 533 IILITSLIGGGLILILITVAYGL 556

RESULT 10  
ABP54363  
ID ABP54363 standard; Protein; 661 AA.

AC ABP54363;

DT 20-JAN-2003 (first entry)

XX Human NR10.3 splicing variant protein SEQ ID NO:2.

XX NR10; splicing variant; haematopoietin receptor; immunomodulator;  
KW haemostatic; haematopoietic factor; immunological disease;  
KW haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

PN WO200277230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

PT (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

DR WPI; 2003-018925/01.

DR N-PSDB; ABQ83363.

XX NR10 splicing variants of hematopoietin receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -

PS Example 2; Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors, and developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietin receptor genes participate  
CC in *in vivo* immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence represents the human NR10.3  
CC protein from the present invention.

XX Sequence 681 AA;

Query Match 100.0%; Score 109; DB 24; Length 681;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILILITVAYGL 24  
Db 552 IILITSLIGGGLILILITVAYGL 575

RESULT 11

ABP05730

ID ABB05730 standard; Protein; 732 AA.

XX ABB05730;

DT 01-MAY-2002 (first entry)

DE Human zcytor17 protein sequence SEQ ID NO:2.

XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
KW antinflammatory; antiviral; antineuritic; antitachytic; cytostatic;  
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

PN WO200200721-A2.

PD 03-JAN-2002.

PF 26-JUN-2001; 2001WO-US20484.

PR 26-JUN-2000; 2000US-214282P.

PR 29-JUN-2000; 2000US-214955P.

PR 08-FEB-2001; 2001US-267963P.

PA (ZYMO) ZYMOGENETICS INC.

PI Sprecher CA, Pressnell SR, Gao Z, Whitmore TE, Kuljper JL;

PI Maurer MF;

DR WPI; 2002-090519/12.

DR N-PSDB; ABA93767.

PS Claim 18; Page 166-168; 235pp; English.

XX The present invention describes a cytokine receptor designated zcytor17.  
CC zcytor17 has immunomodulatory, antinflammatory, antiviral, cytostatic,  
CC antirheumatic, antitachytic and muscular activities. The zcytor17  
CC proteins are useful for treating and diagnosing lymphoid, immune,  
CC inflammatory, splenic, blood or bone disorders. Agonists or  
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
CC immunity and for stimulating lymphocyte proliferation, such as in the  
CC treatment of infections involving immunosuppression, including certain  
CC viral infections. They are also useful for inducing cytotoxicity and  
CC for treating leukopenias. Antagonists of zcytor17 polypeptides are useful  
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
CC pancreaticitis, and inflammatory bowel disease. Zcytor17 was mapped to  
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
CC exemplification of the present invention.

XX Sequence 732 AA;

Query Match 100.0%; Score 109; DB 23; Length 732;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILILITVAYGL 24  
Db 520 IILITSLIGGGLILILITVAYGL 543

RESULT 12

AAE24024  
ID AAE24024 standard; Protein; 745 AA.

XX

AAE24024;  
 23-SEP-2002 (first entry)  
 Human haematopoietin receptor 1 (HPR1) protein.  
 Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;  
 pancytopenia; leucopenia; anaemia; thrombocytopenia; osteoporosis;  
 neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
 cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
 ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
 osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;  
 anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
 demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
 vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
 stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 ischemic disease.  
 Homo sapiens.  
 Location/Qualifiers  
 20..32  
 /label=Signal\_peptide  
 33..745  
 /note="Human mature HPR1 protein"  
 33..241  
 /note="Cytokine receptor domain"  
 83  
 /note="This residue changes to Ala during  
 allelic variation"  
 135..138  
 /note="Proline-rich linker"  
 139..241  
 /note="C-terminal cytokine receptor subdomain"  
 168  
 /note="This residue changes to Asn during  
 allelic variation"  
 187  
 /note="This residue changes to Thr during  
 allelic variation"  
 224..228  
 /note="WSXWS motif"  
 242..515  
 /note="Fibronectin repeat"  
 361  
 /note="This residue changes to Pro during  
 allelic variation"  
 362  
 /note="This residue changes to Gly during  
 allelic variation"  
 510  
 /note="This residue changes to Asn during  
 allelic variation"  
 517  
 /note="Encoded by GAC. This residue changes to  
 Asp during allelic variation"  
 526..556  
 /note="Extended transmembrane domain"  
 533..552  
 /note="Core transmembrane domain"  
 553..745  
 /note="Cytoplasmic domain"  
 563..573  
 /note="Box1 conserved motif"  
 588..592  
 /note="Repeat peptide"  
 597..601  
 /note="Repeat peptide"  
 603..607  
 /note="Repeat peptide"  
 614..618  
 /note="Repeat peptide"  
 619..623

FT Domain /note="Repeat peptide"  
 631..641  
 /note="Box2 conserved motif"  
 FT Region 635..639  
 /note="Repeat peptide"  
 FT Misc-difference 679  
 /note="This residue changes to Gly during  
 allelic variation"  
 PN MO200229060-A2.  
 PD 11-APR-2002.  
 PP 05-OCT-2001; 2001WO-US31634.  
 PR 06-OCT-2000; 2000US-238706P.  
 PR 13-OCT-2000; 2000US-240476P.  
 PR 20-FEB-2001; 2001US-270282P.  
 XX (IMMW ) IMMUNEX CORP.  
 PA Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR.  
 PI WPI; 2002-330172/36.  
 DR N-PSDB; AAD38772.  
 XX Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 XX hormone related conditions -  
 XX Claim 1; Page 84-87; 136pp; English.

XX The present invention relates to human and murine haematopoietin receptor  
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leucopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukaemia and tumour  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related conditions. They are useful for treating various haematologic and  
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such  
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polynuropathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC myasthenia gravis, chronic neuronal degeneration, stroke including  
 CC cerebral ischemic diseases. HPR1 and HPR2 polypeptides are also useful  
 CC for treating various other disorders such as osteoporosis, obesity,  
 CC deficient mammary development and infertility. The present sequence  
 CC is human HPR1 protein.

XX Sequence 745 AA;

Query Match 100.0%; Score 109; DB 23; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILLITLGGGLIIIIITVAYGL 24  
 |||

Db 533 ILITSLIGGGLILILITVAYGL 556

# RESULT 13

ABP54364  
ID ABP54364 standard; Protein; 764 AA.

XX AC ABP54364;

XX DT 20-JAN-2003 (first entry)

XX DE Human NR10.4 splicing variant protein SEQ ID NO:4.

XX NM NR10; splicing variant; haematopoietic receptor; immunomodulator;

XX KW haemostatic; haematopoietic factor; immunological disease;

XX KM haematopoietic disease; haematopoietic cell regulation.

XX OS Homo sapiens.

XX PN MO200277230-A1.

XX PD 03-OCT-2002.

XX PF 22-MAR-2002; 2002WO-JP02769.

XX PR 26-MAR-2001; 2001JP-0087298.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Maeda M, Yaguchi N, Hasegawa M;

XX DR WPI; 2003-018925/01.

XX N-PSDB; AB083364.

XX PT NR10 splicing variants of hematopoietic receptor proteins and encoded

XX PT genes, applicable in searching hematopoietic factors and developing

XX PT remedies for immunological and hematopoietic diseases

XX PS Claim 1; Fig 6; 250pp; Japanese.

XX CC The present invention describes haematopoietic receptor NR10 splicing

XX CC variants (I). (I) have immunomodulator and haemostatic activities. The

XX CC proteins and encoded genes are applicable in searching for novel

XX CC haematopoietic factors, and developing remedies for immunological and

XX CC haematopoietic diseases. The haematopoietic receptor genes participate

XX CC in in vivo immunomodulation and haematopoietic cell regulation, and in

XX CC the search for haematopoietic factors capable of functionally binding

XX CC to the receptors. The present sequence represents the human NR10.4

XX CC protein from the present invention.

XX SQ Sequence 764 AA;

XX Query Match 100.0%; Score 109; DB 24; Length 764;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-07;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 552 ILITSLIGGGLILILITVAYGL 575

XX 1 ILITSLIGGGLILILITVAYGL 24

XX IIILITSLIGGGLILILITVAYGL 575

## RESULT 14

ABP54365  
ID ABP54365 standard; Protein; 764 AA.

XX AC ABP54365;

XX DT 20-JAN-2003 (first entry)

XX DE Human NR10.4 splicing variant protein SEQ ID NO:6.

XX NM NR10; splicing variant; haematopoietic receptor; immunomodulator;

XX KW haemostatic; haematopoietic factor; immunological disease;

KW haematopoietic disease; haematopoietic cell regulation.

XX OS Homo sapiens.

XX PN MO200277230-A1.

XX PD 03-OCT-2002.

XX PF 22-MAR-2002; 2002WO-JP02769.

XX PR 26-MAR-2001; 2001JP-0087298.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Maeda M, Yaguchi N, Hasegawa M;

XX DR WPI; 2003-018925/01.

XX N-PSDB; AB083365.

XX PT NR10 splicing variants of hematopoietic receptor proteins and encoded

XX PT genes, applicable in searching hematopoietic factors and developing

XX PT remedies for immunological and hematopoietic diseases

XX PS Claim 1; Fig 7-9; 250pp; Japanese.

XX CC The present invention describes haematopoietic receptor NR10 splicing

XX CC variants (I). (I) have immunomodulator and haemostatic activities. The

XX CC proteins and encoded genes are applicable in searching for novel

XX CC haematopoietic factors, and developing remedies for immunological and

XX CC haematopoietic diseases. The haematopoietic receptor genes participate

XX CC in in vivo immunomodulation and haematopoietic cell regulation, and in

XX CC the search for haematopoietic factors capable of functionally binding

XX CC to the receptors. The present sequence represents the human NR10.4

XX CC protein from the present invention.

XX SQ Sequence 764 AA;

XX Query Match 100.0%; Score 109; DB 24; Length 764;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-07;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 552 ILITSLIGGGLILILITVAYGL 575

XX 1 ILITSLIGGGLILILITVAYGL 24

XX IIILITSLIGGGLILILITVAYGL 575

XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;

XX KW antiinflammatory; antiviral; antirheumatic; antileukemic; cytostatic;

XX KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;

XX KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;

XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;

XX KW inflammatory disease; pancreatitis; inflammatory bowel disease.

XX OS Mus musculus.

XX PN WO200200721-A2.

XX PD 03-JAN-2002.

XX PF 26-JUN-2001; 2001WO-US20484.

XX PR 26-JUN-2000; 2000US-214282P.

XX PR 29-JUN-2000; 2000US-214955P.

PR 08-FEB-2001; 2001US-267963P.

XX (ZYMO) ZYMOGENETICS INC.  
PA  
NY

PI Sprechter CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;  
PI Maurer MF;

Maurer MF;

XX WPT : 2003 000F10/13  
DB

DR ME1; 2002-090519/  
DR N-PSDB; ABA93810.  
xx

PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
PT splenic, blood or bone disorders -

splenic, blood or bone disorders -

PS Example 21; Page 212-213; 235pp; English..

The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antineoplastic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93467 to ABA93443 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

exemplification of the present invention.

**SQ Sequence 662 AA;**

|                       |              |          |              |            |
|-----------------------|--------------|----------|--------------|------------|
| Query Match           | 76.1%        | Score 83 | DB 23        | Length 662 |
| Best Local Similarity | 66.7%        | Pred     | No. 0.00085  |            |
| Matches 16            | Conservative | 5        | Mismatches 3 | Indels 0   |
|                       |              |          | Gaps         | 0          |

Indels 3; Mismatches 5; Conservative 16; Indels 3; Mismatches 5; Conservative 16;

0.

1 IILITSLIGGLILITVAYGL 24

Db 534 IVLLTSLVGGGLLSIKVTTFGL 557

Search completed: August 18, 2003, 13:27:02  
Job time : 10.1211 secs

Job time : 10.1211 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:24:23 ; Search time 2.96437 Seconds  
(without alignments)  
342.555 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_520\_543

Perfect score: 109

Sequence: 1 ILITSLIGGGLLIILTVAYGL 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                         |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1          | 49    | 45.0        | 337    | 1     | US-08-153-848-46 Sequence 46, Appl  |
| 2          | 49    | 45.0        | 337    | 3     | US-09-299-843A-46 Sequence 46, Appl |
| 3          | 49    | 45.0        | 337    | 4     | US-09-088-337B-46 Sequence 46, Appl |
| 4          | 49    | 45.0        | 337    | 5     | PCT-US93-11153-46 Sequence 46, Appl |
| 5          | 49    | 45.0        | 352    | 1     | US-08-202-056-3 Sequence 3, Appl    |
| 6          | 49    | 45.0        | 352    | 1     | US-08-076-093A-4 Sequence 4, Appl   |
| 7          | 49    | 45.0        | 352    | 1     | US-08-701-265-4 Sequence 4, Appl    |
| 8          | 49    | 45.0        | 352    | 2     | US-08-284-586-4 Sequence 4, Appl    |
| 9          | 49    | 45.0        | 352    | 2     | US-08-805-478-4 Sequence 4, Appl    |
| 10         | 49    | 45.0        | 352    | 2     | US-08-802-627A-4 Sequence 4, Appl   |
| 11         | 49    | 45.0        | 352    | 2     | US-08-801-238-4 Sequence 4, Appl    |
| 12         | 49    | 45.0        | 352    | 2     | US-08-801-228-4 Sequence 4, Appl    |
| 13         | 49    | 45.0        | 352    | 3     | US-09-104-296-4 Sequence 4, Appl    |
| 14         | 49    | 45.0        | 352    | 4     | US-09-517-605-4 Sequence 4, Appl    |
| 15         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 16         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 17         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 18         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 19         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 20         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 21         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 22         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 23         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 24         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 25         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 26         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |
| 27         | 49    | 45.0        | 352    | 4     | US-08-118-270-346 Sequence 4, Appl  |

|    |    |      |      |   |  |
|----|----|------|------|---|--|
| 28 | 47 | 43.1 | 459  | 1 | US-08-413-118-12 Sequence 12, Appl     |
| 29 | 47 | 43.1 | 459  | 1 | US-08-413-118-14 Sequence 14, Appl     |
| 30 | 47 | 43.1 | 459  | 3 | US-08-473-446-12 Sequence 14, Appl     |
| 31 | 47 | 43.1 | 459  | 3 | US-08-473-446-14 Sequence 14, Appl     |
| 32 | 47 | 43.1 | 459  | 3 | US-09-213-053-6 Sequence 2, Appl       |
| 33 | 47 | 43.1 | 1394 | 3 | US-09-213-053-2 Sequence 2, Appl       |
| 34 | 46 | 42.2 | 92   | 1 | US-08-118-270-341 Sequence 341, App    |
| 35 | 46 | 42.2 | 92   | 5 | PCT-US93-08528-341 Sequence 26228, A   |
| 36 | 45 | 41.3 | 258  | 4 | US-09-252-991A-26228 Sequence 27195, A |
| 37 | 45 | 41.3 | 296  | 4 | US-09-172-353-2 Sequence 2, Appl       |
| 38 | 45 | 41.3 | 370  | 3 | US-09-172-353-3 Sequence 3, Appl       |
| 39 | 45 | 41.3 | 370  | 3 | US-09-172-353-7 Sequence 7, Appl       |
| 40 | 45 | 41.3 | 370  | 3 | US-08-776-971-140 Sequence 140, App    |
| 41 | 45 | 41.3 | 370  | 3 | US-09-799-955-2 Sequence 2, Appl       |
| 42 | 45 | 41.3 | 370  | 4 | US-09-799-955-3 Sequence 3, Appl       |
| 43 | 45 | 41.3 | 370  | 4 | US-09-799-955-7 Sequence 7, Appl       |
| 44 | 45 | 41.3 | 370  | 4 | US-09-328-352-6288 Sequence 6288, Ap   |
| 45 | 44 | 40.4 | 141  | 4 | US-09-328-352-6288                     |

#### ALIGNMENTS

RESULT 1  
US-08-153-848-46  
Sequence 46, Application US/08153848  
Patent No. 5759804  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153, 848  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5759804and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-153-848-46  
Query Match 45.0%; Score 49; DB 1; Length 337;  
Best Local Similarity 47.1%; Pred. No. 24;  
Matches 8; Conservative 6; Mismatches 0; Gaps 0;

QY 1 ILLITSLIGGLILILI 17  
| : : : : :  
| : : : : :  
Db 32 IIFLTGIVGNGLVILWM 48

## RESULT 2

US-09-299-843A-46  
Sequence 46, Application US/09299843A  
Patent No. 6107475  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schwellkart, Vicki L.  
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: J111 E. Un1  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/32059B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-299-843A-46

Query Match 45.0%; Score 49; DB 3; Length 337;  
Best Local Similarity 47.1%; Pred. No. 24;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILLITSLIGGLILILI 17  
| : : : : :  
| : : : : :  
Db 32 IIFLTGIVGNGLVILWM 48

## RESULT 3

US-09-088-337B-46  
Sequence 46, Application US/09088337B  
Patent No. 6348574  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.

Schwellkart, Vicki L.  
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,337B  
FILING DATE: 01-JUN-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6348574and, Greta E.  
REFERENCE/DOCKET NUMBER: 35,302  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-088-337B-46

Query Match 45.0%; Score 49; DB 4; Length 337;  
Best Local Similarity 47.1%; Pred. No. 24;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILLITSLIGGLILILI 17  
| : : : : :  
| : : : : :  
Db 32 IIFLTGIVGNGLVILWM 48

## RESULT 4

PCT-US93-11153-46  
Sequence 46, Application PC/TUS9311153  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schwellkart, Vicki L.  
TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11153  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-11153-46

Query Match 45.0%; Score 49; DB 5; Length 337;  
Best Local Similarity 47.1%; Pred. No. 24;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILII 17  
Db 32 IIFLTGIVGNGLVILVM 48

RESULT 5  
US-08-202-056-3  
Sequence 3, Application US/08202056  
Patent No. 5440021  
GENERAL INFORMATION:  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Hebert, Caroline  
APPLICANT: Kim, Kyung Jin  
APPLICANT: Lee, James  
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,056  
FILING DATE: 25-FEB-1994  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/677211  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: 706P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
US-08-202-056-3

Query Match 45.0%; Score 49; DB 1; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILII 17  
Db 47 IIFLTGIVGNGLVILVM 63

RESULT 6  
US-08-076-093A-4  
Sequence 4, Application US/08076093A  
Patent No. 5543503  
GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan  
APPLICANT: Lee, James  
APPLICANT: Hebert, Caroline  
APPLICANT: Jin Kim, K.  
TITLE OF INVENTION: Antibodies to Human PFAA Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/076,093A  
FILING DATE: 11-Jun-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/677211  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: 706P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-076-093A-4

Query Match 45.0%; Score 49; DB 1; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILII 17  
Db 47 IIFLTGIVGNGLVILVM 63

RESULT 7  
US-08-701-265-4  
Sequence 4, Application US/08701265

Patent No. 5776457  
GENERAL INFORMATION:  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Lee, James  
APPLICANT: Hebert, Caroline  
APPLICANT: Jin Kim, K.  
TITLE OF INVENTION: Antibodies to Human PF4A Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/701,265  
FILING DATE: 22-AUG-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/076093  
FILING DATE: 11-Jun-1993  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/677211  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: 706P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-701-265-4

Query Match 45.0%; Score 49; DB 1; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGLILILI 17  
DB 47 IIFLTGIVNGVILVIM 63

RESULT 8  
US-08-284-586-4  
Sequence 4, Application US/08284586  
Patent No. 5840856  
GENERAL INFORMATION:  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Lee, James  
APPLICANT: Hebert, Caroline  
APPLICANT: Jin Kim, K.  
TITLE OF INVENTION: Antibodies to Human PF4A Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,586  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/076,093A  
FILING DATE: 11-Jun-1993  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/677211  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: 706P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-284-586-4

Query Match 45.0%; Score 49; DB 2; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGLILILI 17  
DB 47 IIFLTGIVNGVILVIM 63

RESULT 9  
US-08-805-478-4  
Sequence 4, Application US/08805478  
Patent No. 5874543  
GENERAL INFORMATION:  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Lee, James  
APPLICANT: Hebert, Caroline  
APPLICANT: Jin Kim, K.  
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/805,478  
FILING DATE: 25-Feb-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284586  
FILING DATE: 10-AUG-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093  
 FILING DATE: 11-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/810782  
 FILING DATE: 19-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P0706P2P1C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-5530  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-805-478-4

Query Match 45.0%; Score 49; DB 2; Length 352;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17  
 DB 47 IIFLTGIVNGGLVILWM 63

RESULT 10  
 US-08-802-627A-4  
 Sequence 4, Application US/08802627A  
 Patent No. 5892017  
 GENERAL INFORMATION:  
 APPLICANT: Lee, James  
 TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/802,627A  
 FILING DATE: 19-Feb-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/284586  
 FILING DATE: 10-AUG-1994  
 PRIOR APPLICATION DATA: 08/076093  
 FILING DATE: 11-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/810782  
 FILING DATE: 19-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P0706P2P1D2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-5530  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-802-627A-4

Query Match 45.0%; Score 49; DB 2; Length 352;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17  
 DB 47 IIFLTGIVNGGLVILWM 63

RESULT 11  
 US-08-801-238-4  
 Sequence 4, Application US/08801238  
 Patent No. 5919896  
 GENERAL INFORMATION:  
 APPLICANT: Lee, James  
 TITLE OF INVENTION: PFAA RECEPTOR  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/801,238  
 FILING DATE: 19-Feb-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/284586  
 FILING DATE: 10-AUG-1994  
 PRIOR APPLICATION DATA: 08/076093  
 FILING DATE: 11-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/810782  
 FILING DATE: 19-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P0706P2P1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-5530  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-801-238-4

US-08-801-238-4

Query Match 45.0%; Score 49; DB 2; Length 352;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17  
 DB 47 IIFLTGIVNGGLVILWM 63

RESULT 12

US-08-801-228-4  
; Sequence 4, Application US/08801228  
; Patent No. 5922541  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF  
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
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; APPLICATION NUMBER: US/08/801,228  
; FILING DATE: 19-Feb-1997  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 08/284586  
; FILING DATE: 10-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/076093  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/810782  
; FILING DATE: 19-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0706P2P1D3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
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; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-801-228-4  
Query Match 45.0%; Score 49; DB 2; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
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Db 47 IIFLTGIVNGVLIVM 63  
RESULT 13  
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; Sequence 4, Application US/09104296  
; Patent No. 6087475  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PF4A Receptors  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA

ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,296  
; FILING DATE: 24-June-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/701265  
; FILING DATE: 22-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/664228  
; FILING DATE: 06-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/076093  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/810782  
; FILING DATE: 19-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0706P2C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
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; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-104-296-4  
Query Match 45.0%; Score 49; DB 3; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
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Db 47 IIFLTGIVNGVLIVM 63  
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US-09-517-605-4  
; Sequence 4, Application US/09517605  
; Patent No. 6391567  
; GENERAL INFORMATION:  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Kwon, Douglas S.  
; APPLICANT: van Kooyk, Yvette  
; APPLICANT: Geljtenbeck, Theo  
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 1049-1-017  
; CURRENT APPLICATION NUMBER: US/09/517,605  
; CURRENT FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-517-605-4  
Query Match 45.0%; Score 49; DB 4; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
QY 1 IILITSLIGGGLLILIT 17

Db 47 IIFLTGIVGGLVLM 63

RESULT 15  
US-08-118-270-346

; Sequence 346, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEWMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY=2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ. ID NO: 346:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-118-270-346

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Db 8 VVILITIGNIIIVIMAVCIY 29

Search completed: August 18, 2003, 13:32:22  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 13:27:13 ; Search time 3.1353 Seconds  
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Title: US-09-892-949-2\_COPY\_520\_543  
Perfect score: 109  
Sequence: 1 ILLITSLIGGGLIILLITVAVGL 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0  
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Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| 1          | 109   | 100.0       | 649    | 11 | US-09-892-949-46    |
| 2          | 109   | 100.0       | 652    | 11 | US-09-972-708-14    |
| 3          | 109   | 100.0       | 652    | 15 | US-10-006-265-2     |
| 4          | 109   | 100.0       | 662    | 11 | US-09-972-708-15    |
| 5          | 109   | 100.0       | 662    | 11 | US-09-892-949-54    |
| 6          | 109   | 100.0       | 662    | 15 | US-10-006-265-17    |
| 7          | 109   | 100.0       | 732    | 11 | US-09-892-949-2     |
| 8          | 109   | 100.0       | 745    | 11 | US-09-972-708-4     |
| 9          | 83    | 75.1        | 662    | 11 | US-09-892-949-57    |
| 10         | 82    | 75.2        | 726    | 11 | US-09-972-708-12    |
| 11         | 57    | 52.3        | 1463   | 15 | US-10-156-761-8893  |
| 12         | 51    | 46.8        | 175    | 15 | US-10-156-761-13642 |
| 13         | 51    | 46.8        | 302    | 12 | US-10-017-161-1052  |
| 14         | 51    | 46.8        | 318    | 10 | US-09-886-055-273   |
| 15         | 51    | 46.8        | 318    | 11 | US-09-804-291-273   |

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|----|------|------|-----|----|---------------------|--------------------|
| 16 | 49.5 | 45.4 | 363 | 10 | US-09-738-626-5615  | Sequence 5615, App |
| 17 | 49   | 45.0 | 270 | 12 | US-10-017-161-856   | Sequence 856, App  |
| 18 | 49   | 45.0 | 352 | 10 | US-09-953-692-2     | Sequence 2, Appl   |
| 19 | 49   | 45.0 | 352 | 10 | US-09-953-717-2     | Sequence 2, Appl   |
| 20 | 49   | 45.0 | 352 | 10 | US-09-104-063-4     | Sequence 4, Appl   |
| 21 | 49   | 45.0 | 352 | 10 | US-09-870-759-37    | Sequence 37, Appl  |
| 22 | 49   | 45.0 | 352 | 10 | US-09-870-759-144   | Sequence 144, App  |
| 23 | 49   | 45.0 | 352 | 12 | US-10-251-703-38    | Sequence 38, Appl  |
| 24 | 49   | 45.0 | 352 | 15 | US-10-235-567A-76   | Sequence 76, Appl  |
| 25 | 49   | 45.0 | 352 | 15 | US-10-245-850-1     | Sequence 1, Appl   |
| 26 | 49   | 45.0 | 397 | 10 | US-09-712-363-280   | Sequence 280, App  |
| 27 | 48   | 44.0 | 18  | 15 | US-10-084-813-127   | Sequence 127, App  |
| 28 | 48   | 44.0 | 24  | 12 | US-10-251-703-39    | Sequence 39, Appl  |
| 29 | 47   | 43.1 | 36  | 11 | US-09-983-802-197   | Sequence 197, App  |
| 30 | 47   | 43.1 | 272 | 9  | US-09-755-456-10    | Sequence 10, Appl  |
| 31 | 47   | 43.1 | 299 | 10 | US-09-886-055-41    | Sequence 41, Appl  |
| 32 | 47   | 43.1 | 299 | 11 | US-09-804-291-41    | Sequence 41, Appl  |
| 33 | 47   | 43.1 | 299 | 12 | US-10-017-161-232   | Sequence 232, App  |
| 34 | 46.5 | 42.7 | 109 | 11 | US-09-764-891-4763  | Sequence 4763, App |
| 35 | 46.5 | 42.7 | 109 | 15 | US-10-091-572-318   | Sequence 318, App  |
| 36 | 46.5 | 42.7 | 192 | 11 | US-09-776-724A-110  | Sequence 110, App  |
| 37 | 46   | 42.2 | 78  | 9  | US-09-864-761-37650 | Sequence 37650, A  |
| 38 | 46   | 42.2 | 93  | 9  | US-09-811-284-250   | Sequence 250, App  |
| 39 | 46   | 42.2 | 158 | 10 | US-09-747-155-218   | Sequence 218, App  |
| 40 | 46   | 42.2 | 275 | 9  | US-09-755-456-9     | Sequence 9, Appl   |
| 41 | 46   | 42.2 | 277 | 9  | US-09-755-456-7     | Sequence 7, Appl   |
| 42 | 46   | 42.2 | 293 | 12 | US-10-017-161-818   | Sequence 818, App  |
| 43 | 46   | 42.2 | 321 | 9  | US-09-815-242-4890  | Sequence 4990, App |
| 44 | 46   | 42.2 | 321 | 9  | US-09-815-242-10635 | Sequence 10635, A  |
| 45 | 46   | 42.2 | 355 | 15 | US-10-237-563-30    | Sequence 30, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-892-949-46  
; Sequence 46, Application US/09892949  
; Publication No. US20030096339A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Preenell, Scott R.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Kuiper, Joseph L.  
; APPLICANT: Maurer, Mark F.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
; FILE REFERENCE: 00-42  
; CURRENT APPLICATION NUMBER: US/09/892,949  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,282  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,955  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/267,963  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 46  
; LENGTH: 649  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-892-949-46

Query Match 100.0%; Score 109; DB 11;  
Best Local Similarity 100.0%; Pred. No. 9.5e-07;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILLITSLIGGGLIILLITVAVGL 24  
DB 520 ILLITSLIGGGLIILLITVAVGL 543

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RESULT 2
US-09-972-708-14
; Sequence 14, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-14

Query Match      100.0%; Score 109; DB 11; Length 652;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      533  ILLITSLIGGGLLIIILITVAYGL 556

RESULT 3
US-10-006-265-2
; Sequence 2, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: JP 11/217797
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-2

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Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-972-708-15
; Sequence 15, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
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; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-15

Query Match      100.0%; Score 109; DB 11; Length 662;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILLITSLIGGGLLIIILITVAYGL 24
Db      533  ILLITSLIGGGLLIIILITVAYGL 556

RESULT 5
US-09-892-949-54
; Sequence 54, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Candy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-54

Query Match      100.0%; Score 109; DB 11; Length 662;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILLITSLIGGGLLIIILITVAYGL 24
Db      533  ILLITSLIGGGLLIIILITVAYGL 556

RESULT 6
US-10-006-265-17
; Sequence 17, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
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; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-17

Query Match          100.0%; Score 109; DB 15; Length 662;
Best Local Similarity 100.0%; Pred. No. 9,7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAYGL 24
Db 533 IILITSLIGGGLIILITVAYGL 556

RESULT 7
US-09-892-949-2
; Sequence 2, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-2

Query Match          100.0%; Score 109; DB 11; Length 732;
Best Local Similarity 100.0%; Pred. No. 1,1e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAYGL 24
Db 520 IILITSLIGGGLIILITVAYGL 543

RESULT 8
US-09-972-708-4
; Sequence 4, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
```

```
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-4

Query Match          100.0%; Score 109; DB 11; Length 745;
Best Local Similarity 100.0%; Pred. No. 1,1e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAYGL 24
Db 533 IILITSLIGGGLIILITVAYGL 556

RESULT 9
US-09-892-949-57
; Sequence 57, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 662
; TYPE: PRT
; ORGANISM: mus musculus
US-09-892-949-57

Query Match          76.1%; Score 83; DB 11; Length 662;
Best Local Similarity 66.7%; Pred. No. 0.0029;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAYGL 24
Db 534 IILITSLIGGGLIILITVAYGL 557

RESULT 10
US-09-972-708-12
; Sequence 12, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
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; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 726  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-972-708-12

Query Match 75.2%; Score 82; DB 11; Length 726;  
Best Local Similarity 62.5%; Pred. No. 0.0043;  
Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILITVAAGL 24  
:::|||||:|:|  
Db 517 VVLTSLVGGGLLILSIKVTFGI 540

RESULT 11  
US-10-156-761-8893  
; Sequence 8893, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMTA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 8893  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-8893

Query Match 52.3%; Score 57; DB 15; Length 463;  
Best Local Similarity 55.6%; Pred. No. 5.7;  
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 ILITSLIGGGLILITL 19  
||:|||||:|:  
Db 235 ILTALIGGIFLVAVT 252

RESULT 12  
US-10-156-761-13642  
; Sequence 13642, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMTA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 13642  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-13642

Query Match 46.8%; Score 51; DB 15; Length 175;  
Best Local Similarity 42.9%; Pred. No. 13;  
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILITVA 21  
:::|||||:|:|  
Db 38 VLVVLLIGGLIGLIVLNSA 58

RESULT 13  
US-10-017-161-1052  
; Sequence 1052, Application US/10017161  
; Publication No. US2003014368A1  
; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 08435/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1052  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-1052

Query Match 46.8%; Score 51; DB 12; Length 302;  
Best Local Similarity 57.9%; Pred. No. 23;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILITL 19  
||:|||||:|:  
Db 35 ISVTRALLGNSLILITL 53

RESULT 14  
US-09-886-055-273  
; Sequence 273, Application US/09886055  
; Patent No. US20020132273A1  
; GENERAL INFORMATION:  
; APPLICANT: STRYER, LUBERT  
; APPLICANT: ZOZULYA, SERGEY  
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND  
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS  
; FILE REFERENCE: 078003-0277150  
; CURRENT APPLICATION NUMBER: US/09/886,055  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,812  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 522  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 273  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-886-055-273

Query Match 46.8%; Score 51; DB 10; Length 318;  
Best Local Similarity 57.9%; Pred. No. 24;

| Matches | 11; Conservative     | 3; Mismatches | 5; Indels | 0; Gaps |
|---------|----------------------|---------------|-----------|---------|
| Qy      | 1 IIILTSLLGGGLLIILT  | 19            |           |         |
|         | :   :                |               |           |         |
| Db      | 35 ISYVALLGNSLLIFILT | 53            |           |         |

```

RESULT 15
US-09-804-291-273
: Sequence 273, Application US/09804291
: Publication No. US2003088059A1
: GENERAL INFORMATION:
: APPLICANT: ZOZULA, SERGEY
: TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
: FILE REFERENCE: P 0278005
: CURRENT APPLICATION NUMBER: US/09/804,291
: PRIOR FILING DATE: 2001-03-13
: PRIOR APPLICATION NUMBER: 60/188,914
: PRIOR FILING DATE: 2000-03-13
: PRIOR APPLICATION NUMBER: 60/192,033
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: 60/198,474
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/199,335
: PRIOR FILING DATE: 2000-04-24
: PRIOR APPLICATION NUMBER: 60/207,702
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/213,849
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/226,534
: PRIOR FILING DATE: 2000-08-16
: PRIOR APPLICATION NUMBER: 60/230,732
: PRIOR FILING DATE: 2000-09-07
: PRIOR APPLICATION NUMBER: 60/266,862
: PRIOR FILING DATE: 2001-02-07
: NUMBER OF SEQ ID NOS: 529
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 273
: LENGTH: 318
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-804-291-273

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|                       |       |              |    |            |    |        |     |
|-----------------------|-------|--------------|----|------------|----|--------|-----|
| Query Match           | 46.8% | Score        | 51 | DB         | 11 | Length | 318 |
| Best Local Similarity | 57.9% | Pred. NO.    | 24 |            |    |        |     |
| Matches               | 11    | Conservative | 3  | Mismatches | 5  | Indels | 0   |
|                       |       |              |    |            |    | Gaps   | 0   |

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QY      1 IILTSLIGGGLLIILT 19
        | :|:| | | | |
Db     35 ISVTALLGNSLLFIILT 53
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Search completed: August 18, 2003, 13:33:24  
Job time : 4.46873 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:23:02 ; Search time 3.36342 Seconds  
(without alignments)  
686.221 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_520\_543  
Perfect score: 109  
Sequence: 1 ILLITSLIGGGLILLITLVAYGL 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 55    | 50.5        | 662    | 2 A54078 | methyl-accepting c  |
| 2          | 52    | 47.7        | 527    | 2 H72536 | probable oligopept  |
| 3          | 51    | 46.8        | 97     | 2 C75415 | hypothetical prote  |
| 4          | 51    | 46.8        | 206    | 2 T34961 | probable membrane   |
| 5          | 51    | 46.8        | 280    | 1 C70784 | probable dihemecy   |
| 6          | 51    | 46.8        | 329    | 2 H64220 | membrane protein m  |
| 7          | 51    | 46.8        | 465    | 2 H87591 | sensor histidine k  |
| 8          | 51    | 46.8        | 530    | 2 E82189 | methyl-accepting c  |
| 9          | 50.5  | 46.3        | 580    | 2 S76846 | hypothetical prote  |
| 10         | 50.5  | 46.3        | 1433   | 1 GNVBDM | M polypeptide prec  |
| 11         | 50    | 45.9        | 366    | 2 G00048 | catenolic amino aci |
| 12         | 49    | 45.0        | 352    | 2 G00048 | fusin (LESTRA) - c  |
| 13         | 49    | 45.0        | 352    | 2 A45747 | neuropeptide Y/pep  |
| 14         | 49    | 45.0        | 353    | 2 S28787 | conserved hypothet  |
| 15         | 49    | 45.0        | 353    | 2 H75265 | histidine kinase-1  |
| 16         | 49    | 45.0        | 368    | 2 A96273 | probable serine pr  |
| 17         | 49    | 45.0        | 368    | 2 A96273 | hypothetical prote  |
| 18         | 49    | 45.0        | 397    | 2 H70789 | hypothetical prote  |
| 19         | 49    | 45.0        | 413    | 2 T23766 | hypothetical prote  |
| 20         | 49    | 45.0        | 455    | 2 A75121 | hypothetical prote  |
| 21         | 49    | 45.0        | 539    | 2 T27559 | hypothetical prote  |
| 22         | 49    | 45.0        | 929    | 2 T32492 | hypothetical prote  |
| 23         | 49    | 45.0        | 1124   | 2 B84742 | probable receptor   |
| 24         | 48.5  | 44.5        | 266    | 2 AB2270 | hypothetical prote  |
| 25         | 48    | 44.0        | 339    | 2 D83201 | probable glycosyl   |
| 26         | 48    | 44.0        | 397    | 2 T44477 | hypothetical prote  |
| 27         | 48    | 44.0        | 401    | 2 F87196 | probable membrane   |
| 28         | 48    | 44.0        | 405    | 2 H83798 | ABC transporter (p  |
| 29         | 48    | 44.0        | 432    | 2 T21880 | hypothetical prote  |

|    |      |      |     |          |                    |
|----|------|------|-----|----------|--------------------|
| 30 | 48   | 44.0 | 505 | 2 B88206 | protein F21D2.3 (  |
| 31 | 47.5 | 43.6 | 398 | 2 B71193 | hypothetical prote |
| 32 | 47.5 | 43.6 | 448 | 2 F82280 | citrate/sodium sym |
| 33 | 47   | 43.1 | 322 | 2 A64023 | hypothetical prote |
| 34 | 47   | 43.1 | 343 | 2 AD1502 | hypothetical prote |
| 35 | 47   | 43.1 | 423 | 2 T26306 | hypothetical prote |
| 36 | 47   | 43.1 | 430 | 2 F70016 | purine permease ho |
| 37 | 47   | 43.1 | 473 | 2 AF1207 | ABC transporters ( |
| 38 | 47   | 43.1 | 662 | 2 D54078 | methyl-accepting c |
| 39 | 46.5 | 42.7 | 446 | 2 A18244 | citrate transport  |
| 40 | 46   | 42.2 | 96  | 2 E69790 | hypothetical prote |
| 41 | 46   | 42.2 | 153 | 2 T17893 | hypothetical prote |
| 42 | 46   | 42.2 | 202 | 2 UC4635 | tumor-associated l |
| 43 | 46   | 42.2 | 202 | 2 JC6205 | cell surface anti  |
| 44 | 46   | 42.2 | 216 | 2 H83757 | hypothetical prote |
| 45 | 46   | 42.2 | 242 | 2 A69026 | conserved hypothet |

## ALIGNMENTS

## RESULT 1

A54078 methyl-accepting chemotaxis protein mcpB - Bacillus subtilis

C/Species: Bacillus subtilis  
C/Date: 06-Jan-1995 #sequence \_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: A54078; H69655

R/Hanlon, D.W., Ordal, G.W.  
J. Biol. Chem. 269, 14038-14046, 1994

A/Title: Cloning and characterization of genes encoding methyl-accepting chemotaxis prot  
A/Reference number: A54078; MUID:94245722; PMID:8188684

A/Accession: A54078  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-662 <HAN>

A/Cross-References: GB:L29189; NID:9459687  
A/Note: The sequence in Genbank entry BACMCPUP, release 106.0. (PID:9459688) has 360-N

R/Kunet, F.; Ogasawara, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berce  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chic  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erttington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

leoh, J.; Harwood, C.R.; Hentut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maue

Y, M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, W.; Sadate, Y.; Sato, T.; Scanlon,  
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seto

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Terogni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, f  
A/Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: H69655  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA  
A/Accession: H69655  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Residues: 1-359, 'N', 361-449, 'G', 451-662 <KUN>  
A/Cross-References: GB:Z99119; GB:Z99120; GB:AL009126; NID:92635613; PIDN:CAB15115.1; PI

A/Experimental source: strain 168  
C/Comment: Strains in which this protein is inactivated are defective in chemotaxis tow  
C/Genetic: C;Gene: mcpB

A/Supfamily: Probable methyl-accepting chemotaxis transducer  
C/Keywords: chemotaxis; signal transduction; transmembrane protein

Query Match 50.5%; Score 55; DB 2; Length 662;  
Best Local Similarity 55.6%; Pred. No. 11;  
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILLITSLIGGGLILLITL 18  
DB 286 IVLINSLVAGGLILITV 303





A/Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*  
A/Reference number: A64300; MUID:96337999; PMID:868087  
A/Accession: C64449  
A/Residues: 1-352 <R>  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-366 <R>  
A/Cross-references: GB:U67561; GB:L77117; NID:92826373; PIDN:AA99200.1; PID:G1591825; T  
C/Genetics:  
A/Map position: REV1140149-1139049  
C/Superfamily: probable cationic amino acid transporter MCAT-2

Query Match 45.0%; Score 50; DB 2; Length 366;  
Best Local Similarity 50.0%; Pred. No. 29;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 ILITSLIGGGLILIT 19  
DB 12 ILITSLIGGGLILIT 29

RESULT 12  
G00048  
fuefn (LESTRA) - crab-eating macaque  
C/Species: Macaca fascicularis (crab-eating macaque)  
C/Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 26-Aug-1999  
C/Accession: G00048  
R/Tatsumi, M.  
Submitted to GenBank, July 1996  
A/Reference number: H00048  
A/Accession: G00048  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-352 <R>  
A/Cross-references: GB:D86579; NID:G1468948; PID:G1468948  
C/Superfamily: vertebrate rhodopsin

Query Match 45.0%; Score 49; DB 2; Length 352;  
Best Local Similarity 47.1%; Pred. No. 37;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILIT 17  
DB 47 ILITSLIGGGLILIT 63

RESULT 13  
A45747  
neuropeptide Y/peptide YY receptor Y3 - human  
N/Alternate names: fushin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re  
C/Species: Homo sapiens (man)  
C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 05-Nov-1999  
C/Accession: A45747; A53103; I53006; I59444; I69203; S32761  
R/Federapfel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis  
Genomics 16, 707-712, 1993  
A/Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu  
A/Reference number: A45747; MUID:93315164; PMID:8325644  
A/Accession: A45747  
A/Molecule type: mRNA  
A/Residues: 1-352 <R>  
A/Cross-references: GB:M92993; NID:G292516; PIDN:AAA16617.1; PID:G292517  
R/Loercher, M.; Gelsner, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.  
J. Biol. Chem. 269, 232-237, 1994  
A/Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e  
A/Reference number: A53103; MUID:94103215; PMID:8276799  
A/Accession: A53103  
A/Molecule type: mRNA  
A/Residues: 1-352 <R>  
A/Cross-references: EMBL:X71635; NID:G297099; PIDN:CAA50641.1; PID:G297100  
R/Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.  
DNA Cell Biol. 12, 465-471, 1993  
A/Title: Molecular cloning, characterization, and localization of the human homolog to  
A/Reference number: I53006; MUID:93319629; PMID:8329116  
A/Accession: I53006

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-352 <R>  
A/Cross-references: GB:U67561; NID:G414929; PIDN:AAA03209.1; PID:G414928  
R/Jazin, E.B.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar  
Regul. Pept. 47, 247-258, 1993  
A/Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo  
A/Reference number: I59444; MUID:94052833; PMID:8234909  
A/Accession: I59444  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-352 <R>  
A/Cross-references: GB:L01639; NID:G189313; PIDN:AAA16594.1; PID:G189314  
R/Nomura, H.; Nielsen, B.W.; Matsushima, K.  
Int. Immunol. 5, 1239-1249, 1993  
A/Title: Molecular cloning of cDNAs encoding a L078 receptor and putative leukocyte chem  
A/Reference number: I54751; MUID:94092629; PMID:7505609  
A/Accession: I69203  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-352 <R>  
A/Cross-references: GB:D10924; NID:G219868; PIDN:BA01722.1; PID:G219869  
C/Genetics:  
A/Gene: GDB:NPYR, NPYR3  
A/Cross-references: GDB:230002; OMIM:162643  
A/Map position: 2q21-2q21  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.0%; Score 49; DB 2; Length 352;  
Best Local Similarity 47.1%; Pred. No. 37;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILIT 17  
DB 47 ILITSLIGGGLILIT 63

RESULT 14  
S28787  
neuropeptide Y/peptide YY receptor Y3 - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 26-Aug-1999  
C/Accession: S28787  
R/Rimland, J.; Xin, W.; Sweetnam, P.; Saljoh, K.; Nestler, E.J.; Duman, R.S.  
Mol. Pharmacol. 40, 869-875, 1991  
A/Title: Sequence and expression of a neuropeptide Y receptor cDNA.  
A/Reference number: S28787; MUID:92100053; PMID:1661837  
A/Accession: S28787  
A/Molecule type: mRNA  
A/Residues: 1-353 <R>  
A/Cross-references: EMBL:M86739  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 45.0%; Score 49; DB 2; Length 353;  
Best Local Similarity 47.1%; Pred. No. 37;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILIT 17  
DB 48 ILITSLIGGGLILIT 64

RESULT 15  
H75265  
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)  
C/Species: *Deinococcus radiodurans*  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C/Accession: H75265  
R/White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vanmathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Mc  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999  
 A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A:Reference number: A75250; MID:20036896; PMID:10567266  
 A:Accession: H75265  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1353 <WHI>  
 A:Cross-references: GB:AE002080; GB:AE000513; NID:96460327; PIDN:AAF12054.1; PID:9646033  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR2513  
 A:Map position: 1

Query Match 45.0%; Score 49; DB 2; Length 353;  
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 Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 ILTSLIGGGLLILITVAY 22  
 Db 268 VILSTRGGSLTYLLITLAY 288

Search completed: August 18, 2003, 13:31:24  
 Job time : 5.36342 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:27 ; Search time 1.82423 Seconds.  
(without alignments)  
618.695 Million cell updates/sec

|                |                              |
|----------------|------------------------------|
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| Perfect score: | 109                          |
| Sequence:      | 1 ILITSLIGGGLILILTWAYGL 24   |

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Searched:      127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : SwiBSProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID          | Description         |
|------------|-------|-------------|--------|----|-------------|---------------------|
| 1          | 55    | 50.5        | 662    | 1  | MCBP_BACSU  | P39215 bacillus s   |
| 2          | 51    | 46.8        | 280    | 1  | QCRC_MYCTU  | Q10366 mycobacter   |
| 3          | 51    | 46.3        | 329    | 1  | V118_MYCGE  | P47434 mycoplasma   |
| 4          | 50.5  | 46.3        | 1433   | 1  | VGIM_BUNYM  | P44505 bunyame      |
| 5          | 49    | 45.0        | 192    | 1  | CCR4_SHEEP  | Q28553 ovis arie    |
| 6          | 49    | 45.0        | 349    | 1  | CCR4_RAT    | Q08555 ratius nor   |
| 7          | 49    | 45.0        | 352    | 1  | CCR4_CERVO  | Q62747 cervocedus   |
| 8          | 49    | 45.0        | 352    | 1  | CCR4_HUMAN  | P30991 homo sapien  |
| 9          | 49    | 45.0        | 352    | 1  | CCR4_MACFA  | Q28474 macaca fass  |
| 10         | 49    | 45.0        | 352    | 1  | CCR4_MACMU  | P79334 macaca muli  |
| 11         | 49    | 45.0        | 352    | 1  | CCR4_PAPAN  | P56441 papio anub   |
| 12         | 49    | 45.0        | 353    | 1  | CCR4_BOVIN  | P25930 bos taurus   |
| 13         | 49    | 45.0        | 353    | 1  | CCR4_FELCA  | P56458 felis silve  |
| 14         | 49    | 45.0        | 359    | 1  | CCR4_MOUSE  | P70658 m c-x-c che  |
| 15         | 47    | 43.1        | 322    | 1  | YC48_HA8IN  | P44136 haemophilu   |
| 16         | 47    | 43.1        | 430    | 1  | PUC6_BACSU  | Q32140 bacillus s   |
| 17         | 47    | 43.1        | 662    | 1  | TLPB_BACSU  | P39217 bacillus s   |
| 18         | 46.5  | 42.7        | 446    | 1  | CTTN_KLEPN  | P31602 klebsiella   |
| 19         | 46    | 42.2        | 202    | 1  | T4S1_MESAU  | P49111 mesocricetu  |
| 20         | 46    | 42.2        | 283    | 1  | YD03_SCHPO  | Q10227 schizosacch  |
| 21         | 46    | 42.2        | 291    | 1  | Y4T0_RH1SN  | Q53192 rhizobium f  |
| 22         | 46    | 42.2        | 321    | 1  | MEAY_ENTFA  | Q07117 enterococcu  |
| 23         | 46    | 42.2        | 353    | 1  | ILB8_GORGO  | Q28452 gorilla gor  |
| 24         | 45    | 41.3        | 144    | 1  | LY05_METUJA | Q60304 methanococc  |
| 25         | 45    | 41.3        | 347    | 1  | CD2_HORSE   | P37998 horse        |
| 26         | 45    | 41.3        | 370    | 1  | GP10_RAT    | Q64121 ratius norv  |
| 27         | 45    | 41.3        | 518    | 1  | G317_DROME  | Q9V776 drosophila   |
| 28         | 45    | 41.3        | 553    | 1  | GPT1_CANAL  | Q74248 candida alb  |
| 29         | 45    | 41.3        | 557    | 1  | UBIB_XANAC  | Q8P641 xanthomonasa |
| 30         | 45    | 41.3        | 557    | 1  | UBIB_XANAC  | Q8P641 xanthomonasa |
| 31         | 44.5  | 40.8        | 379    | 1  | CTI2_ECOLI  | P05853 escherichia  |
| 32         | 44.5  | 40.8        | 481    | 1  | YMBL_BACSU  | P39555 bacillus su  |
| 33         | 44    | 40.4        | 170    | 1  | HEMX_PROMI  | Q51887 proteus milt |

| RESULT 1   | ALIGNMENTS   |
|------------|--|
| MCPB_BACSU |  |
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| AC         | P39215;  |
| DT         | 01-FEB-1995 (Rel. 31, Created)   |
| DT         | 01-FEB-1995 (Rel. 31, Last sequence update)                                  |
| DT         | 28-FEB-2003 (Rel. 41, Last annotation update)                                |
| DE         | Methyl-accepting chemotaxis protein mcpB (H3).                               |
| GN         | MCPB.  |
| OS         | Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.                    |
| OC         | Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.                    |
| OX         | NCBI_TaxId=1423;   |
| LN         | [1]  |
| RP         | SEQUENCE FROM N.A.   |
| RC         | STRAIN=168 / 011085;   |
| RC         | MEDLINE=94254722; PubMed=818664;   |
| RA         | Hanlon D.W., Ordal G.W.;   |
| RT         | "Cloning and characterization of genes encoding methyl-accepting             |
| RT         | chemotaxis proteins in <i>Bacillus subtilis</i> ."                           |
| RL         | J. Biol. Chem. 269:14038-14046(1994).  |
| RN         | [2]  |
| RP         | SEQUENCE FROM N.A.   |
| RC         | STRAIN=168;  |
| RC         | MEDLINE=98044033; PubMed=9384377;  |
| RA         | Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,                |
| RA         | Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchart S.,             |
| RA         | Borries R., Borrer L., Brans A., Brun M., Brignell S.C., Bron S.,            |
| RA         | Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,             |
| RA         | Choi S.K., Codani J.U., Conterton I.F., Cummings N.J., Daniel R.A.,          |
| RA         | Daniot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,           |
| RA         | Erlich K.D., Errington J., Fabret C., Ferrati E., Foulger D.,                |
| RA         | Frutkin K.D., Fujita Y., Fuma S., Gallizzi A., Galleron N.,                  |
| RA         | Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,                |
| RA         | Gutseppe G., Guy B.J., Haga K., Haeche U., Harwood C.R., Henaut A.,          |
| RA         | Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,        |
| RA         | Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,           |
| RA         | Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,              |
| RA         | Kurita K., Lapdus A., Lardinois S., Lauber J., Lazarevic V.,                 |
| RA         | Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,                |
| RA         | Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,          |
| RA         | Neone D., O'Reilly M., Ogawa K., Ogawa R., Oudega B., Park S.H.,             |
| RA         | Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,             |
| RA         | Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,        |
| RA         | Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,               |
| RA         | Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,                 |
| RA         | Sekiguchi J., Sekowska A., Serris S.J., Serris P., Shin B.S.,                |
| RA         | Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,                |
| RA         | Takenuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,              |
| RA         | Tosato V., Uchiyama S., Vandenoit M., Vannier F., Vassartotti A.,            |
| RA         | Vaiari A., Wambutt R., Wedler H., Wedler H., Wetzinger T.,                   |
| RA         | Winters P., Witat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,          |
| RA         | Yoshida K., Yoshikawa H.F., Zunshtein B., Yoshikawa H., Zunshtein A.,        |
| RT         | "The complete genome sequence of the Gram-positive bacterium <i>Bacillus</i> |
| RT         | <i>subtilis</i> ."   |
| RL         | Nature 390:249-256(1997).  |
| CC         | -!- FUNCTION: RESPONSIBLE FOR DETECTING A SUBSET OF AMINO ACIDS THAT         |

CC INCLUDES ASPARAGINE, ASPARTATE, GLUTAMINE, AND HISTIDINE.  
 CC -1- FUNCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE  
 CC CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT,  
 CC TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND  
 CC FACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL  
 CC OF METHYLATION. ALL AMINO ACIDS SERVE AS ATTRACTANTS IN  
 CC B. SUBTILIS, THEY APPEAR TO CAUSE AN INCREASE IN THE TURNOVER  
 CC METHYL GROUPS, LEADING TO METHYLATION OF AN UNIDENTIFIED ACCEPTOR,  
 CC WHILE REPELLENTS HAVE BEEN SHOWN TO CAUSE A DECREASE IN METHYL  
 CC GROUP TURNOVER. THE METHYL GROUPS ARE ADDED BY A METHYLTRANSFERASE  
 CC AND REMOVED BY A METHYLSTERASE.  
 CC -1- SIMILARITY: Contains 1 methyl-accepting transducer domain.  
 CC -1- SIMILARITY: Contains 1 HAM domain.  
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 CC -----  
 DR EMBL; L29189; AAA20554.1; -;  
 DR EMBL; Z99119; CAB15104.1; -;  
 DR EMBL; Z99120; CAB15115.1; -;  
 DR PIR; A54078; A54078.  
 DR HSSP; P02942; 10U7.  
 DR Subtilisin; BG10859; mcpb.  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR004089; Chmexis\_transd.  
 DR InterPro; IPR003660; HAM.  
 DR InterPro; IPR003122; Tarrh.  
 DR Pfam; PF02743; Cache; 1.  
 DR Pfam; PF00672; HAM; 1.  
 DR Pfam; PF00015; MCPsignal; 1.  
 DR Pfam; PF02203; Tarrh; 1.  
 DR SMART; SM00304; HAM; 1.  
 DR SMART; SM00283; MA; 1.  
 DR SMART; SM00319; Tarrh; 1.  
 DR PROSITE; PS50111; CHEMOTAXIS\_TRANSDUC\_2; 1.  
 DR PROSITE; PS50885; HAM; 1.  
 KW Chemotaxis; Transducer; Transmembrane; Methylation; Complete proteome.  
 DR DOMAIN 1 16  
 FT TRANSSEM 1 37  
 FT TRANSSEM 38 282  
 FT TRANSSEM 283 303  
 FT TRANSSEM 304 662  
 FT DOMAIN 304 356  
 FT DOMAIN 375 611  
 FT MOD\_RES 371 371  
 FT MOD\_RES 595 595  
 FT MOD\_RES 630 630  
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 Best Local Similarity 55.6%; Pred. No. 7.2;  
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 ID Q10366;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ubiqulinol-cytochrome C reductase cytochrome C subunit.  
 GN QCRC OR RV2194 OR MT2250 OR MTCY150.05.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37Rv;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigler K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jasele K., Jorgensen A., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF THE UBIQUINOL-CYTOCHROME C COMPLEX  
 CC ARE: CYTOCHROME B, THE RIBOSE PROTEIN AND A CYTOCHROME C SUBUNIT.  
 CC -1- SIMILARITY: SOME, TO CYTOCHROME C.  
 CC -----  
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 CC -----  
 DR EMBL; Z70283; CAA94263.1; -;  
 DR EMBL; AB007071; AAK46536.1; -;  
 DR PIR; C70784; C70784.  
 DR TIGR; MT250; -;  
 DR Tuberculin; RV2194; -;  
 DR InterPro; IPR003088; Cyt CI.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR Pfam; PF00034; cytochrome\_c; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 2.  
 KW Electron transport; Heme; Transmembrane; Complete proteome.  
 FT BINDING 73 73  
 FT BINDING 76 76  
 FT METAL 77 77  
 FT BINDING 174 174  
 FT BINDING 177 177  
 FT METAL 178 178  
 FT TRANSSEM 25 45  
 FT TRANSSEM 258 278  
 SO SEQUENCE 280 AA; 29138 MW; 7A058AE7E12BF713 CRC64;  
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 Best Local Similarity 58.8%; Pred. No. 12;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 IGGGLILITLVAYGL 24  
 DB 25 LSGVLLITLITIGGL 41

RESULT 3  
 ID Y188 MYCGE STANDARD; PRT; 329 AA.  
 AC P47434;  
 RN 11;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable ABC transporter permease protein MG188.  
 GN MG188.  
 OS Mycoplasma genitalium.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 NC NCBI\_TaxID=2097;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=96026346; PubMed=7569993;  
 RA Frazer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,  
 RA Nguyen D.T., Utechtack T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
 RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lucier T.S.,  
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,  
 RT "The minimal gene complement of Mycoplasma genitalium.";  
 RL Science 270:337-403(1995).  
 CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE  
 CC SUBSTRATE ACROSS THE MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM PERMEASE FAMILY. MALFG SUBFAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL; U39698; AAC71407.1; -.  
 CC DR PIR; H64220; H64220.  
 CC DR TIGR; MG188; -.  
 CC DR InterPro; IPR000515; BPD transp.  
 CC DR Pfam; PF00528; BPD transp; 1.  
 CC DR PROSITE; PS00402; BPD TRANSP. INN MEMBR. FALSE NEG.  
 CC KM Hypochemical protein: Transport; Transmembrane; Complete proteome.  
 CC FT TRANSMEM 30 50 POTENTIAL.  
 CC FT TRANSMEM 96 116 POTENTIAL.  
 CC FT TRANSMEM 128 148 POTENTIAL.  
 CC FT TRANSMEM 176 196 POTENTIAL.  
 CC FT TRANSMEM 234 254 POTENTIAL.  
 CC FT TRANSMEM 283 303 POTENTIAL.  
 CC SQ SEQUENCE 329 AA; 37201 MW; 45BFB75ACB8BA25 CRC64;  
 Query Match 46.8%; Score 51; DB 1; Length 329;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 5 TSLIGGGLILILITVAYGL 24  
 DB 282 TNLGAGATLVFLVGLVCYGL 301  
 RESULT 4  
 ID VGLM\_BUNYW STANDARD; PRT; 1433 AA.  
 AC P04505;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE M polypeptide precursor [Contains: Glycoprotein G2; Nonstructural  
 DE protein NS-M; Glycoprotein G1].  
 GN M.

OS Bunyamwera virus.  
 OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.  
 NC NCBI\_TaxID=11573;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86098655; PubMed=3753629;  
 RA Lees J.F., Pringle C.R., Elliott R.M.,  
 RT "Nucleotide sequence of the Bunyamwera virus M RNA segment:  
 RT conservation of structural features in the Bunyavirus glycoprotein  
 RT gene product";  
 RL Virology 148:1-14(1986).  
 CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS  
 CC INCLUDING NONSTRUCTURAL PROTEIN NS-M, GLYCOPROTEIN G1, AND  
 CC GLYCOPROTEIN G2.  
 CC -1- SIMILARITY: BELONGS TO THE BUNYAVIRUSES M POLYPROTEIN FAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL; M11852; AAA42777.1; -.  
 CC DR PIR; A04101; GNVIWM.  
 CC DR InterPro; IPR005167; Bunya\_G1.  
 CC DR InterPro; IPR005168; Bunya\_G2.  
 CC DR Pfam; PF03557; Bunya\_G1; 1.  
 CC DR Pfam; PF03563; Bunya\_G2; 1.  
 CC KM Polypeptide; Glycoprotein; Transmembrane; Nonstructural protein;  
 CC signal.  
 CC FT SIGNAL 1 16  
 CC FT CHAIN 17 1433 M POLYPROTEIN.  
 CC FT CHAIN 17 382 GLYCOPROTEIN G2.  
 CC FT CHAIN 303 477 NONSTRUCTURAL PROTEIN NS-M.  
 CC FT CHAIN 478 1433 GLYCOPROTEIN G1.  
 CC FT TRANSMEM 1382 1409 POTENTIAL.  
 CC FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 1169 1169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SQ SEQUENCE 1433 AA; 162077 MW; CD61ABDE782018E0 CRC64;  
 Query Match 46.3%; Score 50.5; DB 1; Length 1433;  
 Best Local Similarity 62.5%; Pred. No. 49;  
 Matches 15; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 IILITSLGGGLILILITVAYGL 24  
 DB 364 IILYTSLFGAGLTI-IPAGVNLGL 386  
 RESULT 5  
 ID CCR4\_SHEEP STANDARD; PRT; 192 AA.  
 AC Q28553;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)  
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derived  
 DE seven transmembrane domain receptor) (LSTR) (Fragment).  
 GN CXCR4 OR LSTR.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NC NCBI\_TaxID=9940;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hypothalamus;  
 RA Dyer C.J., Mattern R.L., Keisler D.H.;

RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor  
 RT mRNA in the ovine hypothalamus and pituitary."  
 RL Abstr. - Soc. Neurosci. 21:1890-1890(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -1- CAUTION: Was originally (Ref.1) thought to be a receptor for  
 CC neuropeptide Y type 3 (NPY3-R).  
 CC -----  
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 CC -----  
 CC EMBL; U88942; AAA81347.1; -  
 CC Interpro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT NON TER 1 1  
 FT DOMAIN 1 29 1 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 30 53 1 (POTENTIAL).  
 FT TRANSMEM 54 63 1 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 70 89 2 (POTENTIAL).  
 FT DOMAIN 90 100 2 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 122 3 (POTENTIAL).  
 FT DOMAIN 123 144 3 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 145 165 4 (POTENTIAL).  
 FT DOMAIN 166 190 4 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 191 192 5 (POTENTIAL).  
 FT TRANSMEM 191 192 5 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 99 111 1 BY SIMILARITY.  
 FT MOD RES 11 11 1 SULFATION (POTENTIAL).  
 FT NON TER 192 192  
 SQ SEQUENCE 192 AA; 22178 MW; A8BCE930CS2BD98 CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 192;  
 Best Local Similarity 47.1%; Pred. No. 15;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 IILITSLIGGLILILI 17  
 DB 37 IIFLTGIVNGVLIVLM 53  
 RESULT 6  
 CCR4\_RAT STANDARD; PRT; 349 AA.  
 AC 008565;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (stromal cell-  
 DE derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived  
 DE seven transmembrane domain receptor) (LESTR).  
 GN CXCR4 OR CXCR4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WiStar; TISSUE=Spleen;  
 RA Harrison J.K.; Salafraza M.N.;  
 RT "Molecular cloning of rat CXCR4."  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A

CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC INVOLVED IN B-CELL LYMPHOPOIESIS, BONE-MARROW MYELOPOIESIS AND IN  
 CC CARCINOMA VASCULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENTIAL ROLE  
 CC IN VASCULARIZATION OF THE GASTROINTESTINAL TRACT, PROBABLY BY  
 CC REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN  
 CC ENDOTHELIAL CELLS. INVOLVED IN CEREBELLAR NEURONAL LAYER  
 CC FORMATION, PREVENTING PREMATURE MIGRATION OF PROLIFERATING GRANULE  
 CC CELLS FROM THE EXTERNAL GRANULE LAYER INWARDS. IN THE CNS, COULD  
 CC MEDIATE HIPPOCAMPAL-NEURON SURVIVAL (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS AND IN ASTROCYTES.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; U90610; AAB50408.1; -  
 CC Interpro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT NON TER 1 36  
 FT DOMAIN 1 60 1 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 37 76 1 (POTENTIAL).  
 FT TRANSMEM 61 76 2 (POTENTIAL).  
 FT DOMAIN 77 97 2 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 97 107 3 (POTENTIAL).  
 FT DOMAIN 108 129 3 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 130 151 4 (POTENTIAL).  
 FT DOMAIN 152 172 4 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 173 197 5 (POTENTIAL).  
 FT DOMAIN 198 217 5 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 218 237 6 (POTENTIAL).  
 FT DOMAIN 238 258 6 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 259 282 6 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 283 302 7 (POTENTIAL).  
 FT TRANSMEM 303 349 7 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 106 183 4 BY SIMILARITY.  
 FT MOD RES 4 4 4 SULFATION (POTENTIAL).  
 FT MOD RES 18 18 4 SULFATION (POTENTIAL).  
 FT CARBOHYD 8 8 1 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 349 AA; 39334 MW; 7E0789A605C60C09 CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 349;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 IILITSLIGGLILILI 17  
 DB 44 IIFLTGIVNGVLIVLM 60  
 RESULT 7  
 CCR4\_CERTO STANDARD; PRT; 352 AA.  
 AC 062747;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)  
 DE (stromal cell-derived factor 1 receptor) (Fusin) (LESTR).  
 GN CXCR4.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.

OC NCBI\_TaxID=9531;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9831155; PubMed=9656999;  
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;  
 RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys  
 naturally infected in west Africa: a comparison of coreceptor usage  
 of primary HIV, HIV-2, and HIVmac.";  
 RL Virology 246:113-124(1998).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: SUPPRESSED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL AF051906; AAC39834.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_P1\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_P1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 63  
 FT DOMAIN 64 79  
 FT TRANSMEM 80 99  
 FT DOMAIN 100 110  
 FT TRANSMEM 111 132  
 FT DOMAIN 133 154  
 FT TRANSMEM 155 175  
 FT DOMAIN 176 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 240  
 FT TRANSMEM 241 261  
 FT DOMAIN 262 285  
 FT TRANSMEM 286 305  
 FT DOMAIN 306 352  
 FT MOD RES 21 21  
 FT CARBOHYD 11 11  
 FT DISULFID 109 186  
 SQ SEQUENCE 352 AA; 39648 MW; 4027432B8032F87E CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 352;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ILLITSLIGGLILILII 17  
 Db 47 IIFLTGIVGVILVLM 63  
 RESULT 8  
 CCR4 HUMAN STANDARD; PRT; 352 AA.  
 ID P30991; O60835; P56438; O9UKN2;  
 AC P30991; O60835; P56438; O9UKN2;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (stromal cell-  
 derived factor 1 receptor) (SDF-1 receptor) (Fusin) (leukocyte-derived  
 seven transmembrane domain receptor) (LESTR) (LCR1) (PB22) (NPYRL)  
 DE (HM89) (CD184 antigen).  
 GN CXCR4.  
 OS Homo sapiens (Human), and  
 OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606, 9598;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human; TISSUE=Lung;  
 RX MEDLINE=93319629; PubMed=8329116;  
 RA Herzog H., Hott Y.J., Shine J., Selbie L.A.;  
 RT "Molecular cloning, characterization, and localization of the human  
 homolog to the reported bovine NPY Y3 receptor: lack of NPY binding  
 and activation.";  
 RL DNA Cell Biol. 12:465-471(1993).  
 RN (2)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human; TISSUE=Fetal brain;  
 RX MEDLINE=94052833; PubMed=8234909;  
 RA Jazin E.E., Yoo H., Blomqvist A.G., Yee F., Weng G., Walker M.W.,  
 RA Salton J., Lathamar D., Mahlestedt C.R.;  
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its  
 human homologue, confers neither NPY binding sites nor NPY  
 responsiveness on transfected cells.";  
 RL Regul. Pept. 47:247-258(1993).  
 RN (3)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human; TISSUE=Fetal spleen;  
 RX MEDLINE=93315164; PubMed=8325644;  
 RA Federspiel B., Melhado I.G., Duncan A.M., Delaney A.D.,  
 RA Schappert K.T., Clark-Lewis I., Jirik F.R.;  
 RT "Molecular cloning of the cDNA and chromosomal localization of the  
 gene for a putative seven-transmembrane segment (7-TMS) receptor  
 isolated from human spleen.";  
 RL Genomics 16:707-712(1993).  
 RN (4)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human; TISSUE=Monocytes;  
 RX MEDLINE=94103215; PubMed=8276799;  
 RA Loetscher M., Gelsner T., O'Reilly T., Zwaalen R., Baggiolini M.,  
 RA Moser B.;  
 RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that  
 is highly expressed in leukocytes.";  
 RL J. Biol. Chem. 269:232-237(1994).  
 RN (5)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human; TISSUE=Monocytes;  
 RX MEDLINE=94092629; PubMed=7505609;  
 RA Nomura H., Nielsen B.W., Matsushima K.;  
 RT "Molecular cloning of cDNAs encoding a L778 receptor and putative  
 leukocyte chemotactic peptide receptors.";  
 RL Int. Immunol. 5:1239-1249(1993).  
 RN (6)  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION OF ITS HIV-1  
 RP CORECEPTOR FUNCTION.  
 RX MEDLINE=96217947; PubMed=8629022;  
 RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;  
 RT "HIV-1 entry cofactor: functional cDNA cloning of a seven-  
 transmembrane, G protein-coupled receptor.";  
 RL Science 272:872-877(1996).  
 RN (7)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human; TISSUE=Peripheral blood leukocytes;  
 RX MEDLINE=98136183; PubMed=9468539;  
 RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Sleeker A.L.,  
 RA Michel N.L.;  
 RT "Genomic organization and functional characterization of the chemokine  
 receptor CXCR4, a major entry co-receptor for human immunodeficiency  
 virus type 1.";  
 RL J. Biol. Chem. 273:4754-4760(1998).  
 RN (8)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC SPECIES=Human;  
 RX MEDLINE=98258970; PubMed=9599023;  
 RA Caruz A., Samsom M., Alonso J.M., Alcamí J., Balleux F.,  
 RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;

RT "Genomic organisation and promoter characterization of human CXCR4  
RT gene";  
RL FEBS Lett. 426:271-278(1998).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human;  
RX MEDLINE=99408510; PubMed=10480633;  
RA Xiao L., Weiss S.H., Qari S.H., Rudolph D., Zhao C., Denny T.N.,  
RT "Partial resistance to infection by R5/4 primary HIV type 1 isolates  
RT in an exposed-uninfected individual homozygous for CCR5 32-base pair  
RT deletion";  
RL AIDS Res. Hum. Retroviruses 15:1201-1208(1999).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Peritoneal blood lymphocytes;  
RX MEDLINE=99095114; PubMed=9879064;  
RA Froel R., Gierschik P., Moeppe B.;  
RT "Genomic organisation and expression of the CXCR4 gene in mouse and  
RT man: absence of a splice variant corresponding to mouse CXCR4-B in  
RT human tissues";  
RL J. Recept. Signal Transduct. Res. 18:321-344(1998).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC SPECIES=Human; TISSUE=Neutrophils;  
RX MEDLINE=99384048; PubMed=10452968;  
RA Gupta S.K., Pillarsetti K.;  
RT "CXCR4-Lo: molecular cloning and functional expression of a novel  
RT human CXCR4 splice variant";  
RL J. Immunol. 163:2368-2372(1999).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC SPECIES=P.troglodytes;  
RX MEDLINE=98090115; PubMed=9430250;  
RA Pietri J.-L., Zerbib A.C., Girard C., Guillet J.-G., Buton C.;  
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";  
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
RN [13]  
RP SULFATION.  
RC SPECIES=Human;  
RX MEDLINE=99189752; PubMed=10089882;  
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,  
RT Gerard N.P., Gerard C., Sodroski J., Choe H.;  
RN "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
RT entry";  
RL Cell 96:667-676(1999).  
RN [14]  
RP FUNCTION.  
RC MEDLINE=96351077; PubMed=8752280;  
RX Blisul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,  
RA Sodroski J., Springer T.A.;  
RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and  
RL blocks HIV-1 entry";  
RN Nature 382:829-833(1996).  
RN [15]  
RP FUNCTION.  
RC MEDLINE=96351078; PubMed=8752281;  
RX Oberlin E., Amara A., Bachelierie F., Beesla C., Virelizier J.-L.,  
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,  
RA Legler D.P., Loetscher M., Baggiolini M., Moser B.;  
RT "The CXC chemokine SDF-1 is the ligand for LESTR/fusin and prevents  
RT infection by T-cell-line-adapted HIV-1";  
RL Nature 382:833-835(1996).  
RN [16]  
RP ERRATUM.  
RX Arenzana-Seisdedos F., Bachelierie F., Beesla C., Virelizier J.-L.,  
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;  
RL Nature 384:288-288(1996).  
RN [17]  
RP CHARACTERIZATION OF ITS HIV-1 CORECEPTOR FUNCTION.  
RX MEDLINE=97002453; PubMed=8849450;  
RN Lapham C.K., Ouyang J., Chandrasekhar B., Nguyen N.Y., Dimitrov D.S.,

```

RA Golding H.;
RT "Evidence for cell-surface association between fusin and the CD4-gp120
RT complex in human cell lines.";
RL Science 274:602-605(1996).
RN [18]
RP CHARACTERIZATION OF ITS HIV-2 RECEPTOR FUNCTION.
RX MEDLINE=97083584; PubMed=8929542;
RA Hendrie M.J., Clapham P.R., Marsh M., Ahuja M., Turner J.D.,
RA McKnight A., Thomas J.P., Stehnen-Haggarty B., Choe S., Vance P.J.,
RA Wells T.N.C., Power C.A., Sutherland S.S., Dome R.W., Landau N.R.,
RA Hoxie J.A.;
RT "CD4-independent infection by HIV-2 is mediated by fusin/CXCR4.";
RL Cell 87:745-756(1996).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC INVOLVED IN HAEMATOPOIESTIS AND IN CARDIAC VENTRICULAR SEPTUM
CC FORMATION. PLAYS ALSO AN ESSENTIAL ROLE IN VASCULARIZATION OF THE
CC GASTROINTESTINAL TRACT, PROBABLY BY REGULATING VASCULAR BRANCHING
CC AND/OR REMODELLING PROCESSES IN ENDOTHELIAL CELLS. COULD BE
CC INVOLVED IN CEREBELLAR DEVELOPMENT. IN THE CNS, COULD MEDIATE
CC HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME
CC HIV-2 ISOLATES AND AS A CO-RECEPTOR WITH CD4 FOR HIV-1 X4 VIRUSES
CC (LYMPHOCYTE-TROPIC HIV-1 VIRUSES, ALSO CALLED SYNCYTIIUM-INDUCING
CC (SI1) STRAINS). PROMOTES ENV-VERIFIED FUSION OF THE VIRUS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P30991-1; Sequence=Displayed;
CC Name=2; Synonyms=CXCR4-1LO;
CC IsoId=P30991-2; Sequence=VSP_001890;
CC Note=Has been shown to exist only in human so far;
CC -1- TISSUE SPECIFICITY: Expressed in numerous tissues, such as
CC peripheral blood leukocytes, spleen, thymus, spinal cord, heart,
CC placenta, lung, liver, skeletal muscle, kidney, pancreas,
CC cerebellum, cerebral cortex and medulla (in microglia as well as
CC in astrocytes), brain microvascular, coronary artery and umbilical
CC cord endothelial cells. Isoform 1 is predominant in all tissues
CC tested.
CC -1- PTM: SULFATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
QY 1 IIITSLIGSLITLI 17
Db 47 IIFLTIIVGSLVILVM 63

RESULT 9
CCR4_MACFA STANDARD; PRT: 352 AA.
AC Q28474;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)
DE (Stromal cell-derived factor 1 receptor) (Fusin) (L85TR).
GN CXCR4.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Ctenidata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
CX NCBI_TaxId=9541;
RN [1]
RP SEQUENCE FROM N.A.
RL Tatsuami M., Takahashi H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

```

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; D86579; BAA13126.1; -.  
 DR PIR; G00048; G00048.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 63  
 FT DOMAIN 64 79  
 FT TRANSMEM 80 99  
 FT DOMAIN 100 110  
 FT TRANSMEM 111 132  
 FT DOMAIN 133 154  
 FT TRANSMEM 155 175  
 FT DOMAIN 176 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 240  
 FT TRANSMEM 241 261  
 FT DOMAIN 262 285  
 FT TRANSMEM 286 305  
 FT DOMAIN 306 352  
 FT MOD RES 21 21  
 FT CARBOHYD 11 11  
 FT DISULFID 109 186  
 SQ SEQUENCE 352 AA; 39753 MW; 432DA6C11859EF8A CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 352;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 IILITSLIGGGLILII 17  
 DB 47 IIFLTGIVNGVLIVM 63  
 RESULT 10  
 CCR4\_MACMU STANDARD; PRT; 352 AA.  
 AC P79394; 002745; 046428;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (SDF-1 receptor)  
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR).  
 GN CXCR4.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxId=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Indian macaque;  
 RX MEDLINE=97213934; Pubmed=9060623;  
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;  
 RT "Genetically divergent strains of simian immunodeficiency virus use  
 RT CCR5 as a coreceptor for entry."  
 RU J. Virol. 71:2705-2714(1997).  
 RL [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268687; Pubmed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Samson M., Lu Z.-H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains."  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Chinese;  
 RX MEDLINE=95825393; Pubmed=9591719;  
 RA Precet J.-L., Guillet J.-G., Butor C.;  
 RT "New widespread CXCR4 allele in rhesus macaques does not predict  
 RT subspecies or clinical evolution."  
 RL AIDS Res. Hum. Retroviruses 14:639-641(1998).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; U73740; AAC51159.1; -.  
 DR EMBL; U93311; AAB54116.1; -.  
 DR InterPro; IPR001928; AAC39644.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 63  
 FT DOMAIN 64 79  
 FT TRANSMEM 80 99  
 FT DOMAIN 100 110  
 FT TRANSMEM 111 132  
 FT DOMAIN 133 154  
 FT TRANSMEM 155 175  
 FT DOMAIN 176 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 240  
 FT TRANSMEM 241 261  
 FT TRANSMEM 262 285  
 FT TRANSMEM 286 305  
 FT DOMAIN 306 352  
 FT MOD RES 21 21  
 FT CARBOHYD 11 11  
 FT DISULFID 109 186  
 FT CONFLICT 67 67  
 FT CONFLICT 214 214  
 FT CONFLICT 348 348  
 SQ SEQUENCE 352 AA; 39739 MW; EC415E4820699C3F CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 352;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 IILITSLIGGGLILII 17  
 DB 47 IIFLTGIVNGVLIVM 63  
 RESULT 11  
 CCR4\_PAPAN

ID CCR4\_PAPAN STANDARD; PRT; 352 AA.  
AC P56491;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (SDF-1 receptor)  
DE (Stromal cell-derived factor 1 receptor) (Fusin).  
GN CXCR4.  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Papio.  
OC NCBI\_TaxID=9555;  
OX NCBI\_TaxID=9555;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCE A  
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- PTM: SULFATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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DR EMBL; AF031089; AAC63831.1; -;  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR Pfam: PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 39  
FT TRANSSEM 40 63  
FT TRANSSEM 64 79  
FT TRANSSEM 80 99  
FT TRANSSEM 100 110  
FT TRANSSEM 111 132  
FT TRANSSEM 133 154  
FT TRANSSEM 155 175  
FT TRANSSEM 176 200  
FT TRANSSEM 201 220  
FT TRANSSEM 221 240  
FT TRANSSEM 241 261  
FT TRANSSEM 262 285  
FT TRANSSEM 286 305  
FT TRANSSEM 306 352  
FT MOD\_RES 21 21  
FT CARBOHYD 11 11  
FT DISULFID 109 186  
SQ SEQUENCE 352 AA; 39751 MW; 468542E1851265A CRC64;  
Query Match 45.0%; Score 49; DB 1; Length 352;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
Db 1 ILLITSLGGGLILIT 17  
47 IIFLTGIVNGVLIVM 63

DT 26-FEB-2003 (Rel. 41, Last annotation update)  
DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (SDF-1 receptor)  
DE (Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derived  
DE seven transmembrane domain receptor) (LESTR) (LCR1).  
GN CXCR4.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Locust coeruleus;  
RX MEDLINE=92100053; PubMed=161837;  
RA Rimland J., Xin W., Sweetnam P., Sajjoh K., Neatler E.J., Duman R.S.;  
RL "Sequence and expression of a neuropeptide Y receptor cDNA.";  
RL Mol. Pharmacol. 40:869-875(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Werling D.;  
RL "Role of chemokines in respiratory syncytial virus infection.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
-----  
RN [3]  
RP SHOWS THAT IT IS NOT A NPY3-R.  
RX MEDLINE=94052833; PubMed=8234909;  
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,  
RA Salan J., Lathammer D., Mahlestedt C.R.;  
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its  
RT human homologue, confers neither NPY binding sites nor NPY  
RT responsiveness on transfected cells.";  
RL Regul. Pept. 47:247-258(1993).  
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCE A  
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.  
CC -1- PTM: SULFATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -1- CAUTION: Was originally (Ref.1) thought to be a receptor for  
CC neuropeptide Y type 3 (NPY3-R).  
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DR EMBL; M66739; -; NOT ANNOTATED\_CDS.  
DR EMBL; AF399642; AAK94452.1; -;  
DR PIR; S28787; S28787.  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 40  
FT TRANSSEM 41 64  
FT TRANSSEM 65 80  
FT TRANSSEM 81 100  
FT TRANSSEM 101 111  
FT TRANSSEM 112 133  
FT TRANSSEM 134 155  
FT TRANSSEM 156 176  
FT TRANSSEM 177 201  
FT TRANSSEM 202 221  
FT TRANSSEM 222 241  
FT TRANSSEM 242 262  
FT TRANSSEM 263 286  
FT TRANSSEM 287 306  
FT TRANSSEM 307 353  
FT MOD\_RES 22 22  
SQ SEQUENCE 353 AA; 39751 MW; 468542E1851265A CRC64;  
Query Match 45.0%; Score 49; DB 1; Length 353;  
Best Local Similarity 47.1%; Pred. No. 25;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
Db 1 ILLITSLGGGLILIT 17  
47 IIFLTGIVNGVLIVM 63

FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 110 187 BY SIMILARITY.  
 SQ SEQUENCE 353 AA; 39938 MW; 42PFESBC7545505E CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 353;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ILITSLIGGGLILII 17  
 48 IIFLTGIVNGLVILVM 64

Db

RESULT 13  
 CCR4\_FELCA STANDARD; PRT; 353 AA.  
 ID\_CCR4\_FELCA 002700; P79172;  
 AC P56458; F02700; P79172;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)  
 (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR).  
 GN CXCR4.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxId=9685;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97404646; PubMed=9261358;  
 RA Willett B.J.; Picard L.; Hosie M.J.; Turner J.D.; Adema K.,  
 RA Clapham P.R.;  
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human  
 RT immunodeficiency viruses";  
 RL J. Virol. 71:6407-6415(1997).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Willett B.J.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Lerner D.L.; Elder J.H.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99399239; PubMed=10470253;  
 RA Kovacs E.M.; Baxter G.D.; Robinson W.F.;  
 RT "Feline peripheral blood mononuclear cells express message for both  
 RT CXCR and CC type chemokines";  
 RL Arch. Virol. 144:273-285(1999).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; U63558; AAC48852.1; -;  
 DR EMBL; U92795; AAB51765.1; -;  
 DR EMBL; AJ009816; CAA08839.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 41 64 1 (POTENTIAL).  
 FT DOMAIN 65 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 100 2 (POTENTIAL).  
 FT DOMAIN 101 111 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 112 133 3 (POTENTIAL).  
 FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 156 176 4 (POTENTIAL).  
 FT DOMAIN 177 201 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 202 221 5 (POTENTIAL).  
 FT DOMAIN 222 241 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 242 262 6 (POTENTIAL).  
 FT DOMAIN 263 286 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 287 306 7 (POTENTIAL).  
 FT DOMAIN 307 353 CYTOPLASMIC (POTENTIAL).  
 FT MOD RES 22 22 SULFATION (POTENTIAL).  
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 110 187 Q -> H (IN REF. 3).  
 FT CONFLICT 67 67 D -> E (IN REF. 3).  
 FT CONFLICT 263 263  
 SQ SEQUENCE 353 AA; 39935 MW; EA2BD46068A6C05B CRC64;  
 Query Match 45.0%; Score 49; DB 1; Length 353;  
 Best Local Similarity 47.1%; Pred. No. 25;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ILITSLIGGGLILII 17  
 48 IIFLTGIVNGLVILVM 64

Db

RESULT 14  
 CCR4\_MOUSE STANDARD; PRT; 359 AA.  
 ID\_CCR4\_MOUSE 009059; P70233; P70346;  
 AC P70658; O09059; O09062; P70233; P70346;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (Stromal cell-  
 DE derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived  
 DE seven transmembrane domain receptor) (PB-CXR).  
 GN CXCR4 OR LESTR OR CMXR4 OR SDF1R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 [1]  
 RP SEQUENCE FROM N.A. (ISOFORM CXCR4-B).  
 RX STRAIN=C57BL/6J, and 129/Sv; TISSUE=Peritoneal exudate;  
 RC MEDLINE=97113334; PubMed=8955194;  
 RA Heesen M.; Berman M.A.; Benson J.D.; Gerard C.; Dorf M.E.;  
 RT "Cloning of the mouse fusin gene, homologue to a human HIV-1  
 RT co-factor";  
 RL J. Immunol. 157:5455-5460(1996).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM CXCR4-B).  
 RC TISSUE=Pre-B cell;  
 RX MEDLINE=97121456; PubMed=8962122;  
 RA Nagasawa T.; Nakajima T.; Tachibana K.; Iizasa H.; Bleu C.C.;  
 RA Yoshie O.; Matsushima K.; Yoshida N.; Spindler T.A.; Kishimoto T.;  
 RT "Molecular cloning and characterization of a murine pre-B-cell  
 RT growth-stimulating factor/stromal cell-derived factor 1 receptor, a  
 RT murine homolog of the human immunodeficiency virus 1 entry coreceptor  
 RT fusin";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).  
 [3]  
 RP SEQUENCE FROM N.A. (ISOFORM CXCR4-B).  
 RC STRAIN=129/Sv; TISSUE=Thymus;  
 RA Schubel A.; Burgstahler R.; Lipp M.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS CXCR4-A AND CXCR4-B).

RC STRAIN=C57BL/6J x CBA; TISSUE=Thymus;  
 RA MEDLINE=97439495; PubMed=9295051;  
 RX Moeppe B., Frodl R., Rodewald H.-R., Baggiolini M., Gierschik P.;  
 RT "Two murine homologues of the human chemokine receptor CXCR4 mediating  
 RT stromal cell-derived factor 1alpha activation of G12 are  
 RT differentially expressed in vivo.";  
 RL Eur. J. Immunol. 27:2102-2112(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS CXCR4-A AND CXCR4-B).  
 RX MEDLINE=97256574; PubMed=9103415;  
 RA Heesen M., Bernan M.A., Hoepken U.E., Gerard N.P., Dorf M.E.;  
 RT "Alternate splicing of mouse fushi/CXC chemokine receptor-4: stromal  
 RT cell-derived factor-1alpha is a ligand for both CXC chemokine  
 RT receptor-4 isoforms.";  
 RL J. Immunol. 158:3561-3564(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM CXCR4-B).  
 RC STRAIN=C57BL/6; TISSUE=Thymus;  
 RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;  
 RL Submitted (EBB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=99095114; PubMed=9879064;  
 RA Frodl R., Gierschik P., Moeppe B.;  
 RT "Genomic organization and expression of the CXCR4 gene in mouse and  
 RT man: absence of a splice variant corresponding to mouse CXCR4-B in  
 RT human tissues.";  
 RL J. Recept. Signal Transduct. Res. 18:321-344(1998).  
 RN [8]  
 RP FUNCTION.  
 RX MEDLINE=98295994; PubMed=9634237;  
 RA Tachibana K., Hirota S., Iizasa H., Yoshida H., Kawabata K.,  
 RA Katsuka Y., Kitemura Y., Matsushima K., Yoshida N., Nishikawa S.-I.,  
 RA Kishimoto T., Nagasawa T.;  
 RT "The chemokine receptor CXCR4 is essential for vascularization of the  
 RT gastrointestinal tract.";  
 RL Nature 393:591-594(1998).  
 RN [9]  
 RP FUNCTION.  
 RX MEDLINE=98295995; PubMed=9634238;  
 RA Zou Y.-R., Kottmann A.H., Kuroda M., Taniuchi I., Littman D.R.;  
 RT "Function of the chemokine receptor CXCR4 in hematopoiesis and in  
 RT cerebellar development.";  
 RL Nature 393:595-599(1998).  
 RN [10]  
 RP DEVELOPMENTAL STAGE.  
 RC STRAIN=ICR;  
 RX MEDLINE=99410349; PubMed=10479460;  
 RA McGee K.E., Koniski A.D., Malby K.M., McGann J.K., Palle J.;  
 RT "Embryonic expression and function of the chemokine SDF-1 and its  
 RT receptor, CXCR4.";  
 RL Dev. Biol. 213:442-456(1999).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC INVOLVED IN B-CELL LYMPHOPOIESIS, BONE-MARROW MYELOPOIESIS AND IN  
 CC CARDIAC VENTRICULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENTIAL ROLE  
 CC IN VASCULARIZATION OF THE GASTROINTESTINAL TRACT. PROBABLY BY  
 CC REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN  
 CC ENDOTHELIAL CELLS. INVOLVED IN CEREBELLAR NEURONAL LAYER  
 CC FORMATION, PREVENTING PREMATURE MIGRATION OF PROLIFERATING GRANULE  
 CC CELLS FROM THE EXTERNAL GRANULAR LAYER INWARDS. IN THE CNS, COULD  
 CC MEDIATE HIPOCAMPAL-NEURON SURVIVAL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=CXCR4-B; Synonyms=LESTR-B;  
 CC IsoId=970658-1; Sequence=Displayed;  
 CC Name=CXCR4-A; Synonyms=LESTR-A;  
 CC IsoId=970658-2; Sequence=VSP\_001891;  
 CC -1- TISSUE SPECIFICITY: LYMPHOCYTES, MACROPHAGES, NEUTROPHILS,  
 CC MICROGLIAL CELLS AND ASTROCYTES. FOUND IN SPLEEN, THYMUS, BONE  
 CC MARROW, LYMPH NODES AND, AT LOWER LEVELS IN BRAIN, SMALL  
 CC INTESTINE, STOMACH AND KIDNEY. CXCR4-A IS PREDOMINANT IN ALL

CC TISSUES TESTED.  
 CC -1- DEVELOPMENTAL STAGE: HIGH EXPRESSION DURING EMBRYONIC DEVELOPMENT  
 CC DOES NOT SEEM TO BE ASSOCIATED WITH THE DIFFERENTIATION OF ANY  
 CC PARTICULAR CELL TYPE, BUT IS WIDELY UTILIZED WHEN THERE IS A  
 CC REQUIREMENT FOR CELL MOVEMENT. FREQUENTLY ASSOCIATED WITH LESS  
 CC DIFFERENTIATED CELL TYPES AND DOWN-REGULATED WITH SUBSEQUENT  
 CC DIFFERENTIATION. DETECTED IN SITES WITH HAEMOPOIETIC POTENTIAL:  
 CC THE YOLK SAC (7.5, 8.5 AND 12.5 DPC) AND FETAL LIVER (12.5 DPC).  
 CC DURING GASTRULATION. AT 7.2 TO 7.8 DPC, EXPRESSED IN THE MESODERM  
 CC AND THE DERIVATIVE ENDODERM. AS GASTRULATION PATTERN PADS (8.5  
 CC DPC), EXPRESSION IN THE MESODERM IS DOWN-REGULATED, WHILE IT  
 CC BECOMES PREDOMINANT IN NEURAL ECTODERM. ENDODERMAL EXPRESSION IS  
 CC RETAINED IN THE FOREGUT AND LATER IN A SUBSET OF FOREGUT  
 CC DERIVATIVES, INCLUDING THE STOMACH (10.5 DPC), THE CYSTIC DUCTS OF  
 CC THE GALLBLADDER AND THE LUNG EPITHELIUM (12.5 DPC). IN NEURONAL  
 CC TISSUE: AT 10.5 AND 12.5 DPC, EXPRESSED IN THE DORSAL ROOT  
 CC GANGLIA, IN THE VENTRAL MANTLE LAYER OF THE SPINAL CORD (OR BASAL  
 CC PLATES), IN THE HINDRAIN. AT 14.5 DPC, EXPRESSION MORE TIGHTLY  
 CC CONFINED TO THE NEURAL EPITHELIUM LINING THE VENTRICULAR SPACE AND  
 CC TO THE EXTERNAL GRANULAR LAYER OF THE VENTRAL RHOMBIC LIP (THE  
 CC DEVELOPING CEREBELLUM). EXPRESSED IN THE OUTPOCKETING OF THE  
 CC DIVERGENT FLOOR AT 10.5 DPC AND IN THE DEVELOPING THALAMUS AND,  
 CC TO A LESSER EXTENT, THE DEVELOPING HIPOTHALAMUS. AT 14.5 DPC,  
 CC RESTRICTED TO THE REGION WHERE THALAMUS AND HYPOTHALAMUS MEET.  
 CC DETECTED IN A DISCRETE BAND OF CELLS AT THE EDGE OF THE OLFACTORY  
 CC BULB. IN THE VASCULAR SYSTEM: EXPRESSED IN THE ENDOTHELIUM OF  
 CC NUMEROUS BLOOD VESSELS, BUT NOT ALL, AT 10.5, 11.5 AND 12.5 DPC,  
 CC SUCH AS VITELLINE/UMBILICAL VESSELS, CARDIAC VENTRICULAR WALL  
 CC CAPILLARIES, FACIAL VESSELS AND, AT 14.5 DPC, IN THE VASCULATURE  
 CC OF THE HERNIATED GUT. EXPRESSION SEEMS TO BE ASSOCIATED WITH  
 CC EXPANDING VASCULAR NETWORKS. IN THE HEART DEVELOPMENT, EXPRESSED  
 CC AT 10.5 DPC IN THE PRECURSOR TO THE AOROPULMONARY (AP) SEPTUM. AT  
 CC 12.5 DPC, DETECTED IN THE AP SEPTUM AT THE BASE OF THE OUTFLOW  
 CC TRACT AND IN THE ATRIOVENTRICULAR VALVES. DETECTED IN CRANOFACIAL  
 CC ECTODERM FROM 10.5 TO 14.5 DPC. AT 10.5 AND 11.5 DPC, EXPRESSED IN  
 CC THE RATNAKE'S POUCH.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; U59760; AAB07725.1; -  
 CC EMBL; U65580; AAC52953.1; -  
 CC EMBL; D87747; BAA13451.1; -  
 CC EMBL; Z80111; CAB02201.1; -  
 CC EMBL; Z80112; CAB02202.1; -  
 CC EMBL; X9981; CAA67893.1; -  
 CC EMBL; X99582; CAA67894.1; -  
 CC EMBL; AB008083; BAA19187.1; -  
 CC MGD; MG1:109563; CXCR4.  
 CC GO; GO:0007420; P:brain development; IMP.  
 CC GO; GO:0030334; P:regulation of cell migration; IMP.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCR\_RHODOPSIN.  
 CC PROSITE; PS00237; G-PROTEIN\_RECP\_F1\_1; 1.  
 CC PROSITE; PS00262; G-PROTEIN\_RECP\_F1\_2; 1.  
 CC KMW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 CC Alternative splicing;  
 CC FT DOMAIN 1 41  
 CC FT TRANSMEM 42 65  
 CC FT DOMAIN 66 81  
 CC FT TRANSMEM 82 101  
 CC FT DOMAIN 102 112  
 CC FT TRANSMEM 113 134  
 CC FT DOMAIN 135 156  
 CC FT TRANSMEM 157 177  
 CC EXTRACELLULAR (POTENTIAL).  
 CC 1 (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC 2 (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC 3 (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC 4 (POTENTIAL).

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FT DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 227 5 (POTENTIAL).
FT DOMAIN 228 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 268 6 (POTENTIAL).
FT DOMAIN 269 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 312 7 (POTENTIAL).
FT DOMAIN 313 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 111 193 BY SIMILARITY.
FT MOD RES 23 23 SULFATION (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 6 7 Missing (in isoform CXCR4-A).
FT CONFLICT 216 216 /FTId=VSP_001891.
SQ SEQUENCE 359 AA; 40426 MW; 33D1B552A31595B CRC64;

Query Match 45.0%; Score 49; DB 1; Length 359;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGILLIIL 17
Db 49 IIFLTGIVNGVLVLW 65

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RESULT 15
YC48 HAEIN STANDARD; PRT; 322 AA.
AC P44136;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H11248.
GN H11248.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kienle A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudex D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: SOME, TO E.COLI YOHM AND M.JANNASCHIT M1092.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL, U32805; AAC22907.1; -.
CC DR PIR; A64023; A64023.
CC DR TIGR; H11248; -.
CC KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 7 27 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.

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FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 322 AA; 35669 MW; EC1248D2F25A1F47 CRC64;

Query Match 43.1%; Score 47; DB 1; Length 322;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 ITSLIGGILLIILTVAYG 23
Db 291 IYKLIAGIMLPFALSILYG 310

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Search completed: August 18, 2003, 13:27:42  
 Job time : 2.82423 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:47 ; Search time 8.49406 Seconds  
(without alignments)  
729.128 Million cell updates/sec

Title: US-09-892-949-2\_COPY\_520\_543  
Perfect score: 109  
Sequence: 1 ILITSLIGGGLILILITVAYGL 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTRMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 109   | 100.0       | 732    | 4 Q8N117  | Q8N117 homo sapien |
| 2          | 83    | 76.1        | 235    | 11 Q8BSU3 | Q8BSU3 mus musculu |
| 3          | 83    | 76.1        | 716    | 11 Q8K5B1 | Q8K5B1 mus musculu |
| 4          | 83    | 76.1        | 716    | 11 Q8R501 | Q8R501 mus musculu |
| 5          | 52    | 47.7        | 314    | 11 Q8VGY3 | Q8VGY3 mus musculu |
| 6          | 52    | 47.7        | 527    | 17 Q9YBL7 | Q9YBL7 aeropyrum p |
| 7          | 52    | 47.7        | 795    | 5 Q9XZF9  | Q9XZF9 drosophila  |
| 8          | 52    | 47.7        | 795    | 5 Q9VUX9  | Q9VUX9 drosophila  |
| 9          | 52    | 47.7        | 795    | 5 Q9NBK8  | Q9NBK8 drosophila  |
| 10         | 51    | 46.8        | 97     | 16 Q9RUV1 | Q9RUV1 deinococcus |
| 11         | 51    | 46.8        | 163    | 2 Q9ZSV8  | Q9ZSV8 streptomyce |
| 12         | 51    | 46.8        | 206    | 16 Q9SZM5 | Q9SZM5 streptomyce |
| 13         | 51    | 46.8        | 254    | 16 Q8RI00 | Q8RI00 fusobacteri |
| 14         | 51    | 46.8        | 288    | 16 Q8KGC3 | Q8KGC3 chlorodiu   |
| 15         | 51    | 46.8        | 314    | 4 Q8NGK2  | Q8NGK2 homo sapien |
| 16         | 51    | 46.8        | 465    | 16 Q9A4R5 | Q9A4R5 caulobacter |

|    |      |      |     |           |                     |
|----|------|------|-----|-----------|---------------------|
| 17 | 51   | 46.8 | 530 | 16 Q9KRU9 | Q9KRU9 vibrio chol  |
| 18 | 50.5 | 46.3 | 580 | 16 P74642 | P74642 synechocyst  |
| 19 | 50   | 45.9 | 366 | 17 Q58596 | Q58596 methanococc  |
| 20 | 49.5 | 45.4 | 233 | 16 Q8CV70 | Q8CV70 oceanobacti  |
| 21 | 49.5 | 45.4 | 363 | 16 Q8NP90 | Q8NP90 corynebacte  |
| 22 | 49   | 45.0 | 270 | 4 Q8NGK6  | Q8NGK6 homo sapien  |
| 23 | 49   | 45.0 | 272 | 16 Q9ZMS2 | Q9ZMS2 rhizobium m  |
| 24 | 49   | 45.0 | 284 | 16 Q8EWI7 | Q8EWI7 mycoplasma   |
| 25 | 49   | 45.0 | 301 | 8 Q950G6  | Q950G6 spitzellomyc |
| 26 | 49   | 45.0 | 306 | 11 Q8VGP1 | Q8VGP1 mus musculu  |
| 27 | 49   | 45.0 | 331 | 17 Q9H24  | Q9H24 thermoplas    |
| 28 | 49   | 45.0 | 332 | 11 Q62973 | Q62973 ratu         |
| 29 | 49   | 45.0 | 334 | 6 Q9N130  | Q9N130 saimiri boi  |
| 30 | 49   | 45.0 | 334 | 6 Q9N1P2  | Q9N1P2 saquinus ce  |
| 31 | 49   | 45.0 | 334 | 6 Q9N1P4  | Q9N1P4 cercopithe   |
| 32 | 49   | 45.0 | 334 | 6 Q9N1P3  | Q9N1P3 hylobates l  |
| 33 | 49   | 45.0 | 346 | 6 Q9WZM2  | Q9WZM2 nycticebus   |
| 34 | 49   | 45.0 | 346 | 6 Q9WZM3  | Q9WZM3 nycticebus   |
| 35 | 49   | 45.0 | 346 | 6 Q9WZM4  | Q9WZM4 nycticebus   |
| 36 | 49   | 45.0 | 347 | 6 Q9WZP2  | Q9WZP2 mandrillu    |
| 37 | 49   | 45.0 | 347 | 6 Q9WZM5  | Q9WZM5 hylobates c  |
| 38 | 49   | 45.0 | 347 | 6 Q9WZP8  | Q9WZP8 colobus pol  |
| 39 | 49   | 45.0 | 347 | 6 Q9WZP1  | Q9WZP1 mandrillu    |
| 40 | 49   | 45.0 | 347 | 6 Q9WZQ0  | Q9WZQ0 pygathrix n  |
| 41 | 49   | 45.0 | 347 | 6 Q9WZM1  | Q9WZM1 eulemur mac  |
| 42 | 49   | 45.0 | 347 | 6 Q9WZM5  | Q9WZM5 pithecia pi  |
| 43 | 49   | 45.0 | 347 | 6 Q9WZP0  | Q9WZP0 macaca asca  |
| 44 | 49   | 45.0 | 347 | 6 Q9WZM6  | Q9WZM6 callithrix   |
| 45 | 49   | 45.0 | 347 | 6 Q9WZM0  | Q9WZM0 alogueta se  |

## ALIGNMENTS

RESULT 1  
Q8N117 PRELIMINARY; PRT; 732 AA.  
ID Q8N117  
AC Q8N117;  
DT 01-OCT-2002 (TRMBLrel. 22, Created)  
DT 01-OCT-2002 (TRMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)  
DE Gp130-like monocyte receptor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2198187; PubMed=11877449;  
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;  
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals  
Proliferation, and Activates STAT-3 and STAT-5.";  
RL J. Biol. Chem. 277:16831-16836(2002).  
DR EMBL; AF486620; AAM27958.1; -.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR Pfam; PR00041; fn3; 1.  
DR SMART; SM00060; FN3; 3.  
KW Receptor.  
SQ SEQUENCE 732 AA; 82953 MW; 30F84BD3DD9A20E CRC64;  
Query Match 100.0%; Score 109; DB 4; Length 732;  
Best Local Similarity 100.0%; Pred. No. 5,3e-06;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ILITSLIGGGLILILITVAYGL 24  
DB 520 ILITSLIGGGLILILITVAYGL 543  
RESULT 2  
Q8BSU3 PRELIMINARY; PRT; 235 AA.

AC OBBUSJ; 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=Pituitary;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK030512; BAC26698.f.1; -.  
KM Hypothetical protein.  
SQ SEQUENCE 235 AA; 25133 MW; 50928397A1AD126F CRC64;

|                     |              |                   |               |             |
|---------------------|--------------|-------------------|---------------|-------------|
| ery Match           | 76.1%;       | Score 83;         | DB 11;        | Length 235; |
| st Local Similarity | 66.7%;       | Pred. No. 0.0043; |               |             |
| atches 16;          | Conservative | 5;                | Mismatches 3; | Indels 0;   |
|                     |              |                   | Gaps          | 0;          |

| QY                         | DB                          |
|----------------------------|-----------------------------|
| 1 IILTSLIGGGLLIILTWAYGL 24 | 26 IVLTLVGGGLLISIKVTYFGL 49 |

RESULT 3  
Q8K5B1  
ID Q8K5B1 PRELIMINARY; PRT; 716 AA

|    |  |   |
|----|--|---|
| DT | 01-OCT-2002  | (TREMblrel. 22, Created)                |
| DT | 01-OCT-2002  | (TREMblrel. 22, Last sequence update)   |
| DT | 01-OCT-2002  | (TREMblrel. 22, Last sequence update)   |
| DT | 01-MAR-2003  | (TREMblrel. 23, Last annotation update) |
| DE | Gp130-like monocyte receptor.  |   |
| GN | GLMR.  |   |
| OS | Mus musculus (Mouse).  |   |
| OC | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |   |
| OC | Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.   |   |
| OX | NCBI_TaxID=10090;  |   |
| RN | [1]  |   |
| RP | SEQUENCE FROM N.A.   |   |
| RX | MEDLINE=21968187; PubMed=11877449;                                   |   |
| RA | Ghilaedi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.,   |   |
| RT | "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals |   |
| RT | Proliferation, and Activates STAT-3 and STAT-5."                     |   |
| RL | J. Biol. Chem. 277:15831-16636(2002).                                |   |
| DR | EMBL; AF486621; AA027959.1; --                                       |   |
| DR | MGI; MGI:2180511; Glnr.  |   |
| DR | InterPro; IPR002996; CRA.  |   |
| DR | InterPro; IPR003961; FN_III.   |   |
| DR | Pfam; PF00041; fn3.1.  |   |
| DR | SMART; SM00060; FN3.3.   |   |
| KM | Receptor.  |   |
| QO | SEQUENCE 716 AA; 80641 MW; 3956B0B253F7C7B5 CRC64;                   |   |

Query Match 76.1%; Score 83; DB 11; Length 716;  
Best Local Similarity 66.7%;  
Best Match 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILITSLIGGGLILILLTVAYGL 24  
Db 507 ILLTSLVGGGLLISIKVTFTGL 530

|            |              |
|------------|--------------|
| RESULT 4   |              |
| Q8R501     |              |
| ID Q8R501  | PRELIMINARY; |
| AC Q8R501; | PRT; 716 AA. |

```

01-JUN-2002 (Tremblrel. 21, Created)
01-JUN-2002 (Tremblrel. 21, last sequence update)
01-OCT-2002 (Tremblrel. 22, last annotation update)
Cytokine receptor NR10.
GN GLMR OR NR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
SEQUENCE FROM N.A..
RP STRAIN=C57BL/6;.
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine
RL receptor NR10." ;
DR Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083111; BAB88745.1; -.
DR MGD; MG1:2180511; Glmr.
DR InterPro; IPR002966; CRAI.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00044; fn3, 1.
DR SMART; SM0060; FN3; 3.
KW Receptor.
OQ SEQUENCE 716 AA; 80598 MW; CBFBY1BDCCD40FC7 CRC64;

Query Match          76.1%; Score 83; DB 11; Length 716;
Best Local Similarity 66.7%; Pred.No. 0.011;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

      1 ILITSLGGGLILILTYAYGL 24
      |:|:|||||||:|:|:|:|
      507 ILVLTSLVGGLLISIKTVFGL 530

```

|                          |       |                  |           |             |
|--------------------------|-------|------------------|-----------|-------------|
| Query Match              | 76.1% | Score 83;        | DB 11;    | Length 716; |
| Best Local Similarity    | 66.7% | Pred. No. 0.011; |           |             |
| Matches 16; Conservative | 5;    | Mismatches 3;    | Indels 0; | Gaps 0;     |

```

QY      1 IILTSLIGGGLLILITVAYGL 24
          |::|||:||||:|:|:|
Db      507 IVLTSLVGGGLLLSLIKVTFL 530

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|           |                          |
|-----------|--------------------------|
| RESULT 5  |                          |
| Q8VGY3    |                          |
| ID Q8VGY3 | PRELIMINARY; PRT; 314 AA |

|    |   |   |
|----|---|---|
| DT | 01-MAR-2002   | (TREMblrel. 20, Created)                |
| DT | 01-MAR-2002   | (TREMblrel. 20, Last sequence update)   |
| DT | 01-MAR-2003   | (TREMblrel. 23, Last annotation update) |
| DE | Olfactory receptor MOR1-4.  |   |
| OS | Mus musculus (Mouse).   |   |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |   |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus |   |
| OX | NCBI_TaxId=10090;   |   |
| RN | [1]   |   |
| RP | SEQUENCE FROM N.A.  |   |
| RA | Zhang X., Firestein S.J.;   |   |
| RT | "The olfactory receptor gene superfamily of the mouse.";          |   |
| RL | Nat. Neurosci. 0:0-0(2002).                                       |   |
| RN | [2]   |   |
| RP | SEQUENCE FROM N.A.  |   |
| RA | Adams M.;   |   |
| RL | Submitted (JAN-2002) to the EMBL/GenBank/DBD databases.           |   |
| DR | EMBL, AY073007; AA60670.1; -;                                     |   |
| DR | InterPro; IPR000276; GPCR_Rhodopsn.                               |   |
| DR | Pfam; PF00001; 7cm.1; 1.  |   |
| DR | PRINTS; PR00237; GPCRRIODOPSN.                                    |   |
| DR | PROSITE; PS00237; G_PROTEIN_RECPT_F1.1; 1.                        |   |
| DR | PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.                        |   |
| QO | RECEPT. 314 AA; 35532 MW; 6308508DD931B80E CRC64;                 |   |
| QO | SEQUENCE  |   |

|                       |       |              |    |            |    |        |     |
|-----------------------|-------|--------------|----|------------|----|--------|-----|
| Query Match           | 47.7% | Score        | 52 | DB         | 11 | Length | 314 |
| Best Local Similarity | 63.2% | Pred. No.    | 53 |            |    |        |     |
| Matches               | 12    | Conservative | 2  | Mismatches | 5  | Indels | 0   |
|                       |       |              |    | Gaps       | 0  |        | 0   |

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QY      1 IILTSLIGGHLIILT 19
        | ||:|:| ||||
Db      35 ISYITALGNSLIIFIILT 53
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RESULT 6
Q9YBL7 PRELIMINARY; PRT; 527 AA.
AC Q9YBL7;
DT 01-NOV-1999 (TRMBLrel. 12, Created)
DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE 527AA long hypothetical oligopeptide transport system permease
DE protein.
GN APE1581.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatakeyama Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaei A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000062; BAA80581.1; -
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR000566; Lipocin_cycFMBP.
DR Pfam: PF00528; BPD_transp; 1.
DR PROSITE: PS00213; LIPOCALIN; 1.
KW Complete proteome.
SQ SEQUENCE 527 AA; 57790 MW; 9120E07F292D6AE1 CRC64;

Query Match 47.7%; Score 52; DB 17; Length 527;
Best Local Similarity 40.9%; Pred. No. 83;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ILIITSLLGGGLLIILITLVAY 22
Db 375 LILFAIILGGNIWVILFIVAF 396

RESULT 7
Q9XZF9 PRELIMINARY; PRT; 795 AA.
AC Q9XZF9;
DT 01-NOV-1999 (TRMBLrel. 12, Created)
DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE TOLL like protein.
GN TEHAO OR CG7121.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RA Luo C., Zheng L.;
RT "Toll and related proteins from insects."
RT Submitted (APR-1999) to the EMBL/GenBank/DBD databases.
DR EMBL: AF140019; AAD30131.1; -
DR HSP: O60603; IFTW.
DR Flybase: FBgn0026760; Tehao.
DR InterPro: IPR004075; IL1_receptor1.
DR InterPro: IPR001611; LRR-
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR000157; TIR_domain.
DR Pfam: PF00560; LRR; 5.
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DR Pfam: PF01462; LRRNT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTERKINRIE.
DR PRINTS: PRO0019; LEURICHRPT.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50506; LRR_TYPICAL; 1.
DR PROSITE: PS50104; TIR; 1.
SQ SEQUENCE 795 AA; 90256 MW; 32288BC66A86E249 CRC64;

Query Match 47.7%; Score 52; DB 5; Length 795;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 ILIITSLLGGGLLIILITLVAY 22
Db 591 VLLISCVGGLVIVICLLTVFY 612

RESULT 8
Q9VUX9 PRELIMINARY; PRT; 795 AA.
AC Q9VUX9;
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE TEHAO protein.
GN TEHAO OR CG7121.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hinkley R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harts N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jafarizadeh S., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodaira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Mohtrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Patel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard Y., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Switkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003640; AAF53306.1; -.  
DR HSSP; O60603; 1FVW.  
DR FlyBase; FBgn0026760; Tehao.  
DR InterPro; IPR004075; IL1\_receptor1.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_Typ.  
DR InterPro; IPR000157; TIR\_domain.  
DR Pfam; PF00560; LRR\_5.  
DR Pfam; PF01462; LRRNT; 1.  
DR Pfam; PF01582; TIR; 1.  
DR PRINTS; PRO1537; INTRLNRI1F.  
DR PRINTS; PRO0019; LEURICHRPT.  
DR SMART; SM00013; LRRNT; 1.  
DR SMART; SM00369; LRR\_Typ; 2.  
DR SMART; SM00255; TIR; 1.  
DR PROSITE; PS50506; LRR\_TYPICAL; 1.  
DR PROSITE; PS50104; TIR; 1.  
SQ SEQUENCE 795 AA; 90241 MW; 61B8839E2036E28C CRC64;

Query Match 47.7%; Score 52; DB 5; Length 795;  
Best Local Similarity 36.4%; Pred. No. 1.2e+02;  
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

OY 1 IILITSLGGGLIILITVAVY 22  
DB 591 VLLISCVGGLVIVICLITVY 612

## RESULT 9

O9NBK8 PRELIMINARY; PRT; 795 AA.

AC O9NBK8; 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Toll-5.  
GN TEHAO OR CG7121.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tauszig S., Jouanguy E., Hoffmann J., Imler J.L.;  
RT "Toll-related receptors and the control of antimicrobial peptide  
expression in Drosophila."  
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).  
DR EMBL; AF247767; AAF66227.1; -.  
DR HSSP; O60603; 1FVW.  
DR FlyBase; FBgn0026760; Tehao.  
DR InterPro; IPR004075; IL1\_receptor1.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_Typ.  
DR InterPro; IPR000157; TIR\_domain.  
DR Pfam; PF00560; LRR\_5.  
DR Pfam; PF01462; LRRNT; 1.  
DR Pfam; PF01582; TIR; 1.  
DR PRINTS; PRO1537; INTRLNRI1F.  
DR PRINTS; PRO0019; LEURICHRPT.  
DR SMART; SM00013; LRRNT; 1.  
DR SMART; SM00369; LRR\_Typ; 2.  
DR SMART; SM00255; TIR; 1.  
DR PROSITE; PS50506; LRR\_TYPICAL; 1.  
DR PROSITE; PS50104; TIR; 1.  
SQ SEQUENCE 795 AA; 90255 MW; 3A0883BE4A66E247 CRC64;

Query Match 47.7%; Score 52; DB 5; Length 795;

Best Local Similarity 36.4%; Pred. No. 1.2e+02;  
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

OY 1 IILITSLGGGLIILITVAVY 22  
DB 591 VLLISCVGGLVIVICLITVY 612

## RESULT 10

O9RUV1 PRELIMINARY; PRT; 97 AA.

AC O9RUV1; 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
DE Hypothetical protein DR1280.  
GN DR1280.  
OS Deinococcus radiodurans.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
OC Deinococcaceae; Deinococcus.  
OX NCBI\_TaxID=1299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RI;  
RX MEDLINE=20036896; PubMed=10567266;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.J., Lam P., McDonald L., Ueberlack T., Zalewski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus  
radiodurans RI."  
RL Science 286:1571-1577(1999).  
DR EMBL; AE001975; AAF10855.1; -.  
DR TIGR; DR1280; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 97 AA; 10260 MW; 1784AF83FFCD5F16 CRC64;

Query Match 46.8%; Score 51; DB 16; Length 97;  
Best Local Similarity 41.7%; Pred. No. 25;  
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 IILITSLGGGLIILITVAVYGL 24  
DB 67 IYILGFVIGSVLALVALAAVYGL 90

## RESULT 11

O9ZSV8 PRELIMINARY; PRT; 163 AA.

AC O9ZSV8; 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE Hypothetical 16.4 kDa protein (Fragment).  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Cadwallader A.B., McCormick J.R.;  
RT "Identification and Characterization of the Cell Division Gene ftsI of  
Streptomyces coelicolor A3(2)."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF123319; AAD20009.1; -.  
DR InterPro; IPR002965; P-rich\_extensn.  
DR PRINTS; PRO1217; PRICHEXTENSN.  
KW Hypothetical protein.  
FT NON\_TER 1

SO SEQUENCE 163 AA; 16354 MW; 09ED9F39D9514B5E CRC64;

Query Match  
Best Local Similarity 46.8%; Score 51; DB 2; Length 163;  
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLIILITVA 21  
12 VLLVVVLLGGGLIGLIVLNSA 32

RESULT 12

Q9S2W5 PRELIMINARY; PRT; 206 AA.

AC Q9S2W5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Putative membrane protein.  
GN SCO2091 OR SC4A10.24C.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
NCBI\_Taxid=1902;

RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Saunders D.C., Harris D.;  
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Redenbach M., Kleiser H.M., Denapalae D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RL "A set of ordered cosmid and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RA MEDLINE=2196410; PubMed=1200953;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL939111; CAB52000.1; -;  
DR InterPro; IPR002965; P rich extensn.  
DR PRINTS; PRO1217; PRICHXTEHNSN.  
KW Complete proteome.  
SQ SEQUENCE 206 AA; 20899 MW; 90131DF9AAB059D7 CRC64;

Query Match  
Best Local Similarity 46.8%; Score 51; DB 16; Length 206;  
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLIILITVA 21  
55 VLLVVVLLGGGLIGLIVLNSA 75

RESULT 13  
Q8RI00 PRELIMINARY; PRT; 254 AA.

AC Q8RI00;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Glycerol uptake facilitator protein.  
GN FN1838.

OS Fusobacterium nucleatum (subsp. nucleatum).  
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
OC Fusobacterium.  
NCBI\_Taxid=76856;

RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 25586;  
RX MEDLINE=21886394; PubMed=11889109;  
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,  
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,  
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,  
RA Larsen N., d'Souza M., Walunas T., Pusch G., Haselkorn R.,  
RA Fontein M., Kyriades N., Overbeek R.;  
RT "Genome sequence and analysis of the oral bacterium Fusobacterium  
nucleatum strain ATCC 25586.";  
RL J. Bacteriol. 184:2005-2018(2002).  
DR EMBL; AE010486; AAL93937.1; -;  
DR InterPro; IPR00425; MIP\_family.  
DR Pfam; PF00230; MIP; 1.  
DR ProDom; PD000295; MIP\_family; 1.  
DR TIGRFAMs; TIGR00861; MIP; 1.  
DR PROSITE; PS00221; MIP; 1.  
KW Complete proteome.

SO SEQUENCE 254 AA; 26879 MW; 8A2618C889339CB2 CRC64;

Query Match  
Best Local Similarity 46.8%; Score 51; DB 16; Length 254;  
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 3 ILITSLIGGGLIILITVAYG 23  
148 IYTEITIGLALLIGVLAIGYG 168

RESULT 14

Q8KGC3 PRELIMINARY; PRT; 288 AA.

AC Q8KGC3;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein CT0045.  
GN CT0045.

OS Chlorobium tepidum.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium.  
NCBI\_Taxid=1097;

RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 49652 / DSM 12025;  
RX MEDLINE=22103685; PubMed=12093901;  
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,  
RA Dodson R.J., Deboy R., Gwin M.L., Nelson W.C., Haft D.H.,  
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,  
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,  
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,  
RA Vamathavan J., Khouiri H., White O., Gruber T.M., Ketchum K.A.,  
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;  
RT "The complete genome sequence of Chlorobium tepidum TDS, a  
photosynthetic, anaerobic, green-sulfur bacterium.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).  
DR EMBL; AE012784; AAM71293.1; -;  
DR TIGR; CT0045; -;

